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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:38:20 ; Search time 89.6501 Seconds
(without alignments)
1488.535 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPIIYNFLSGCKEKSILVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqpl980s:*
2: geneseqpl990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%						
Result		Query						
No.	Score	Match	Length	DB	ID		Description	
1	1947	100.0	372	4	AAU00440		Aau00440 Human neu	
2	1944	99.8	377	2	AAW06126		Aaw06126 Neuropept	
3	1943	99.8	389	2	AAW80805		Aaw80805 Amino aci	
4	1943	99.8	389	4	AAU11187		Aau11187 Human G p	
5	1943	99.8	389	5	ABB08208		Abb08208 G-protein	
6	1903	97.7	369	2	AAW06125		Aaw06125 Neuropept	
7	1903	97.7	425	2	AAW80456		Aaw80456 G-protein	
8	1903	97.7	425	4	AAU11188		Aau11188 Human G p	
9	1903	97.7	425	4	AAU11186		Aau11186 Human G p	

10	1903	97.7	425	4	AAB67079	Aab67079	Human	HFG
11	1903	97.7	425	5	AAG78345	Aag78345	Human	HFG
12	1903	97.7	425	6	ABP81941	Abp81941	Human	ore
13	1903	97.7	425	7	ABG75058	Abg75058	Human	ore
14	1903	97.7	425	7	ADK52564	Adk52564	Hematolog	
15	1903	97.7	425	8	ADL22443	Adl22443	Human	ore
16	1903	97.7	425	8	ADL22428	Adl22428	Human	ore
17	1903	97.7	425	8	ADO29106	Ado29106	Human	nov
18	1898	97.5	425	4	ABB56378	Abb56378	Non-endog	
19	1897	97.4	425	4	AAU00438	Aau00438	Human	neu
20	1897	97.4	425	4	AAB67489	Aab67489	Amino aci	
21	1896	97.4	402	2	AAW06124	Aaw06124	Neuropept	
22	1886.5	96.9	401	5	AAG78346	Aag78346	Human	HFG
23	1875	96.3	369	4	AAU00439	Aau00439	Human	neu
24	1870	96.0	425	4	AAE04740	Aae04740	Cynomolgo	
25	1810	93.0	364	4	AAU00442	Aau00442	Human	neu
26	1785	91.7	416	8	ADO29107	Ado29107	Mouse	nov
27	1783	91.6	427	4	AAB47300	Aab47300	Dog	orexi
28	1347.5	69.2	444	4	AAB61968	Aab61968	Canine	wi
29	1344.5	69.1	444	4	AAB84416	Aab84416	Amino aci	
30	1343.5	69.0	443	8	ADO29110	Ado29110	Mouse	nov
31	1342.5	69.0	460	4	AAB61970	Aab61970	Rat	HCRTR
32	1342.5	69.0	460	6	ABG73515	Abg73515	Rat	OX2R
33	1341.5	68.9	444	4	AAB98007	Aab98007	Human	hyp
34	1341.5	68.9	444	4	AAB61969	Aab61969	Human	HCR
35	1341.5	68.9	444	6	ABG73514	Abg73514	Human	OX2
36	1341.5	68.9	444	6	ABP81942	Abp81942	Human	ore
37	1341.5	68.9	444	7	ABG75059	Abg75059	Human	ore
38	1341.5	68.9	444	8	ADO29109	Ado29109	Human	nov
39	1340.5	68.8	444	2	AAU03649	Aay03649	Human	7-t
40	1336.5	68.6	444	4	ABB56379	Abb56379	Non-endog	
41	1307	67.1	263	2	AAR91233	Aar91233	Rabbit	G-
42	1307	67.1	263	2	AAW11236	Aaw11236	G-protein	
43	1161.5	59.7	330	4	AAB61971	Aab61971	Canine	na
44	994	51.1	327	4	AAB61972	Aab61972	Canine	na
45	495.5	25.4	430	8	ADJ87508	Adj87508	Murine	re

ALIGNMENTS

RESULT 1

AAU00440

ID AAU00440 standard; protein; 372 AA.

XX

AC AAU00440;

XX

DT 18-JUN-2001 (first entry)

XX

DE Human neuropeptide receptor splice variant 2.

XX

KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW cardiovascular disorder; autoimmune disorder; infectious disorder;
KW eating behaviour disorder; narcolepsy; neurological disease;
KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW protein co-ordinate data.

XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 47. .72
 FT /label= TM1
 FT /note= "Transmembrane region 1"
 FT Region 83. .106
 FT /label= TM2
 FT /note= "Transmembrane region 2"
 FT Region 112. .142
 FT /label= TM3
 FT /note= "Transmembrane region 3"
 FT Region 163. .189
 FT /label= TM4
 FT /note= "Transmembrane region 4"
 FT Region 214. .239
 FT /label= TM5
 FT /note= "Transmembrane region 5"
 FT Region 299. .327
 FT /label= TM6
 FT /note= "Transmembrane region 6"
 FT Region 335. .363
 FT /label= TM7
 FT /note= "Transmembrane region 7"
 XX
 PN WO200117532-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 07-SEP-2000; 2000WO-US024518.
 XX
 PR 10-SEP-1999; 99US-00393696.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 2001-183276/18.
 DR N-PSDB; AAS00493.
 XX
 PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
 PT useful for preventing, treating or ameliorating obesity, narcolepsy,
 PT neurological disease and addiction to narcotics, nicotine and alcohol.
 XX
 PS Claim 3; Fig 6; 385pp; English.
 XX
 CC The present sequence represents human neuropeptide receptor splice
 CC variant 2. Two splice variants (AAU00439-AAU00440) and a possible mutant
 CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
 CC described. The neuropeptide receptor shows sequence homology to the
 CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
 CC neuropeptide receptor are useful for diagnosing, preventing, or treating
 CC a pathological condition in a subject related to the central nervous and
 CC peripheral nervous systems (CNS and PNS). The polypeptides and
 CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
 CC autoimmune, nervous system or infectious disorders e.g. cancer, heart

CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
 CC diabetes mellitus. In particular they are useful for preventing, treating
 CC or ameliorating a medical condition in a mammal such as obesity/eating
 CC behaviour disorders, narcolepsy, neurological disease, addiction to
 CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
 CC headaches and anxiety disorders. The polynucleotides encoding the
 CC neuropeptide receptor can also be used in gene therapy methods for
 CC treating such diseases
 XX
 SQ Sequence 372 AA;

Query Match 100.0%; Score 1947; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 1.6e-191;
 Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSAIVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSAIVRNWKRPSDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSGCKEKSIVLS	372
Db	361	LSGCKEKSIVLS	372

RESULT 2

AAW06126

ID AAW06126 standard; protein; 377 AA.

XX

AC AAW06126;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-2.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 46. .71
 FT /note= "Transmembrane region-1"
 FT Domain 82. .104
 FT /note= "Transmembrane region-2"
 FT Domain 110. .140
 FT /note= "Transmembrane region-3"
 FT Domain 160. .186
 FT /note= "Transmembrane region-4"
 FT Domain 210. .235
 FT /note= "Transmembrane region-5"
 FT Domain 293. .321
 FT /note= "Transmembrane region-6"
 FT Domain 329. .356
 FT /note= "Transmembrane region-7"
 XX
 PN WO9634877-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 05-MAY-1995; 95WO-US005616.
 XX
 PR 05-MAY-1995; 95WO-US005616.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 1996-506094/50.
 DR N-PSDB; AAT42828.
 XX
 PT Human neuro-peptide receptor polypeptide(s) - used to identify
 PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
 PT obesity, Alzheimer's disease, epilepsy, etc.
 XX
 PS Disclosure; Page 52-53; 77pp; English.
 XX
 CC The sequence represents human adult hypothalamus neuropeptide receptor
 CC splice variant-2, which retains activity corresponding to the mature
 CC receptor (AAW06124), which is structurally related to the G-protein-
 CC coupled receptor family. The receptor variant contains 7 transmembrane
 CC regions. The receptor may be produced in recombinant form and used in a
 CC drug screening assay for isolation of receptor-agonists and -antagonists,
 CC which may be used as anorectic, antitumour, anticholesterolemic,
 CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
 CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
 CC The receptor itself and its corresponding antibody may also be used in
 CC therapy and diagnosis
 XX
 SQ Sequence 377 AA;

 Query Match 99.8%; Score 1944; DB 2; Length 377;
 Best Local Similarity 99.7%; Pred. No. 3.2e-191;

Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
      |||||||:|||||
Db      1 MEPSATPGAQMGVPPGSRDPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPPQA 180
      |||||||
Db    121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||||||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGCKEKSIVLS 372
      |||||||
Db    361 LSGCKEKSIVLS 372
```

RESULT 3

AAW80805

ID AAW80805 standard; protein; 389 AA.

XX

AC AAW80805;

XX

DT 29-JAN-1999 (first entry)

XX

DE Amino acid sequence of HFGAN72Y a G-protein coupled receptor.

XX

KW G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;

KW antagonist; activation; inhibition; gene therapy; antibody;

KW immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;

KW asthma; Parkinson's disease; acute heart failure; hypotension;

KW² hypertension; urinary retention; osteoporosis; angina pectoris;

KW myocardial infarction; ulcer; allergies; psychotic disorder;

KW neurological disorder; gene mapping.

XX

OS Homo sapiens.

XX

PN EP875565-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308554.

XX

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVLVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTTFSHWLVIYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVLVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTTFSHWLVIYANSAANPIIYNF 360
 Qy 361 LSGCKEKSLLVS 372
 |||||||| ||
 Db 361 LSGCKEKSLLVS 372

RESULT 4

AAU11187

ID AAU11187 standard; protein; 389 AA.

XX

AC AAU11187;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72Y.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72Y; bacterial infection;
 KW fungal infection; protozoan infection; viral infection;
 KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
 KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
 KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
 KW obesity; Kallman's syndrome; hypothalamic disorder;
 KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
 KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

XX
PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.
XX
PS Claim 8; Fig 3; 75pp; English.
XX
CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.
CC infections such as bacterial, fungal, protozoan and viral infections,
CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
CC Huntington's disease and many other diseases and disorders given in the
CC specification. The present sequence is the human HFGAN72Y receptor being
CC the product of a splice variant of HFGAN72
XX
SQ Sequence 389 AA;

Query Match 99.8%; Score 1943; DB 4; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.3e-191;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSGCKEKSILVLS	372

Db ||||| ||
361 LSGCKEKS LALS 372

RESULT 5

ABB08208

ID ABB08208 standard; protein; 389 AA.

XX

AC ABB08208;

XX

DT 12-MAR-2002 (first entry)

XX

DE G-protein coupled receptor (HFGAN72Y).

XX

KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW schizophrenia; manic depression; dementia; mental retardation;
KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2.

XX

OS Homo sapiens.

XX

PN EP1156110-A2.

XX

PD 21-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203010.

XX

PR 30-APR-1997; 97US-00846705.

PR 27-OCT-1997; 97EP-00308554.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-084320/12.

DR N-PSDB; ABA96019.

XX

PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.

XX

PS Claim 10; Page 7; 22pp; English.

XX

CC The sequence represents G-protein coupled receptor HFGAN72Y. The
CC invention relates to a novel isolated polynucleotide encoding HFGAN72Y
CC polypeptide. The polypeptide of the invention has cytostatic, cardiant,
CC analgesic, tranquillising, nootropic, neuroprotective, and anti-asthmatic
CC activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
CC expression is used to treat a subject in need of decreased HFGAN72Y
CC activity or expression. HFGAN72Y-associated diseases include infections,

CC particularly by HIV-1 or HIV-2, cancers, anorexia, bulimia, Parkinson's
CC disease, cardiac diseases, ulcers, urinary retention, asthma, allergies,
CC benign prostatic hypertrophy, and psychotic and neurological disorders
CC including anxiety, schizophrenia, manic depression, delirium, dementia,
CC severe mental retardation and dyskinesias such as Huntington's disease
CC and Tourette's syndrome, and pain

XX

SQ Sequence 389 AA;

Query Match 99.8%; Score 1943; DB 5; Length 389;
Best Local Similarity 99.7%; Pred. No. 4.3e-191;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
|
Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
|
Db 61 LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
|
Db 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|
Db 181 AVMECSSVLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|
Db 241 KLWGRQIPGTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|
Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSIVLS 372
|
Db 361 LSGCKEKSIVLS 372

RESULT 6

AAW06125

ID AAW06125 standard; protein; 369 AA.

XX

AC AAW06125;

XX

DT 22-FEB-1997 (first entry)

XX

DE Neuropeptide receptor splice variant-1.

XX

KW Human; neuropeptide receptor; splice variant; drug screening;

KW receptor-agonist; receptor-antagonist; anorectic; antitumour;

KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;

KW sedative; diagnostic; gene therapy.

XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 47. .72
 FT /note= "Transmembrane region-1"
 FT Domain 83. .106
 FT /note= "Transmembrane region-2"
 FT Domain 112. .142
 FT /note= "Transmembrane region-3"
 FT Domain 163. .189
 FT /note= "Transmembrane region-4"
 FT Domain 214. .239
 FT /note= "Transmembrane region-5"
 FT Domain 299. .327
 FT /note= "Transmembrane region-6"
 FT Domain 335. .363
 FT /note= "Transmembrane region-7"
 XX
 PN WO9634877-A1.
 XX
 PD 07-NOV-1996.
 XX
 PF 05-MAY-1995; 95WO-US005616.
 XX
 PR 05-MAY-1995; 95WO-US005616.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Soppet DR, Li Y, Rosen CA;
 XX
 DR WPI; 1996-506094/50.
 DR N-PSDB; AAT42827.
 XX
 PT Human neuro-peptide receptor polypeptide(s) - used to identify
 PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
 PT obesity, Alzheimer's disease, epilepsy, etc.
 XX
 PS Disclosure; Page 51-52; 77pp; English.
 XX
 CC The sequence represents human adult hypothalamus neuropeptide receptor
 CC splice variant-1, which retains activity corresponding to the mature
 CC receptor (AAW06124), which is structurally related to the G-protein-
 CC coupled receptor family. The receptor variant contains 7 transmembrane
 CC regions. The receptor may be produced in recombinant form and used in a
 CC drug screening assay for isolation of receptor-agonists and -antagonists,
 CC which may be used as anorectic, antitumour, anticholesterolemic,
 CC neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
 CC encoding DNA may be used in genetic disease diagnosis or gene therapy.
 CC The receptor itself and its corresponding antibody may also be used in
 CC therapy and diagnosis
 XX
 SQ Sequence 369 AA;

Query Match 97.7%; Score 1903; DB 2; Length 369;
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
 |||
 Db 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 |||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
 |||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 7

AAW80456

ID AAW80456 standard; protein; 425 AA.

XX

AC AAW80456;

XX

DT 26-JAN-1999 (first entry)

XX

DE G-protein coupled receptor (HFGAN72X) polypeptide.

XX

KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;

KW bulimia; asthma; Parkinson's disease; acute heart failure;

KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;

KW benign prostatic hypertrophy; neurological disorder.

XX

OS Homo sapiens.

XX

PN EP875566-A2.

XX

PD 04-NOV-1998.

XX

PF 27-OCT-1997; 97EP-00308563.

XX

PR 30-APR-1997; 97US-00846704.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX
DR WPI; 1998-559432/48.
DR N-PSDB; AAV63468.
XX
PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.
XX
PS Claim 1; Page 7-8; 24pp; English.
XX
CC The present sequence represents a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X
CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSPVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Db	61	LVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK	120
Qy	121	VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 8

AAU11188

ID AAU11188 standard; protein; 425 AA.

XX

AC AAU11188;

XX

DT 25-FEB-2002 (first entry)

XX

DE Human G protein-coupled receptor HFGAN72X variant.

XX

KW Human; G protein-coupled receptor; GPCR; HFGAN72X; bacterial infection;

KW fungal infection; protozoan infection; viral infection;

KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;

KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;

KW angina pectoris; renal disease; depression; schizophrenia; anorexia;

KW obesity; Kallman's syndrome; hypothalamic disorder;

KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;

KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.

XX

OS Homo sapiens.

XX

PN US2001025031-A1.

XX

PD 27-SEP-2001.

XX

PF 06-APR-2001; 2001US-00828538.

XX

PR 08-JUN-1998; 98US-0088524P.

PR 22-JUL-1998; 98US-0093726P.

PR 08-JUN-1999; 99US-00328014.

XX

PA (ELLI/) ELLIS C E.

PA (KWOK/) KWOK C.

PA (BODS/) BODSWORTH N J.

PA (HALS/) HALSEY W.

PA (HORN/) HORN S V.

XX

PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;

XX

DR WPI; 2001-624968/72.

DR N-PSDB; AAS17464.

XX

PT Isolated HFGAN72 receptor useful for treatment of a patient having need
PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
PT infections such as bacterial, fungal, protozoan and viral infections and
PT cancers.

XX

PS Claim 23; Fig 6; 75pp; English.

XX

CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
CC its variant, encoded by the 8 exon sequences given in the specification.
CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
CC administered by providing to the patient DNA encoding HFGAN72 and
CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
CC useful for applications in the detection and treatment of disease, e.g.

KW fungal infection; protozoan infection; viral infection;
 KW human immunodeficiency virus; HIV; cancer; diabetes; Parkinson's disease;
 KW osteoporosis; myocardial infarction; ulcer; asthma; allergy;
 KW angina pectoris; renal disease; depression; schizophrenia; anorexia;
 KW obesity; Kallman's syndrome; hypothalamic disorder;
 KW idiopathic hormone deficiency; gigantism; migraine; pain; lung disease;
 KW burn; sleep disorder; jet lag; Huntington's disease; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN US2001025031-A1.
 XX
 PD 27-SEP-2001.
 XX
 PF 06-APR-2001; 2001US-00828538.
 XX
 PR 08-JUN-1998; 98US-0088524P.
 PR 22-JUL-1998; 98US-0093726P.
 PR 08-JUN-1999; 99US-00328014.
 XX
 PA (ELLI/) ELLIS C E.
 PA (KWOK/) KWOK C.
 PA (BODS/) BODSWORTH N J.
 PA (HALS/) HALSEY W.
 PA (HORN/) HORN S V.
 XX
 PI Ellis CE, Kwok C, Bodsworth NJ, Halsey W, Horn SV;
 XX
 DR WPI; 2001-624968/72.
 XX
 PT Isolated HFGAN72 receptor useful for treatment of a patient having need
 PT of HFGAN72 receptor and in the detection and treatment of disease, e.g.
 PT infections such as bacterial, fungal, protozoan and viral infections and
 PT cancers.
 XX
 PS Claim 8; Fig 2; 75pp; English.
 XX
 CC The invention relates to an isolated polypeptide, the HFGAN72 receptor or
 CC its variant, encoded by the 8 exon sequences given in the specification.
 CC HFGAN72 is a G protein-coupled receptor (GPCR). HFGAN72 is useful for the
 CC treatment of a patient having need of HFGAN72 receptor where HFGAN72 is
 CC administered by providing to the patient DNA encoding HFGAN72 and
 CC expressing HFGAN72 in vivo (i.e by gene therapy). HFGAN72 is particularly
 CC useful for applications in the detection and treatment of disease, e.g.
 CC infections such as bacterial, fungal, protozoan and viral infections,
 CC particularly infections caused by human immunodeficiency virus (HIV)-1 or
 CC HIV-2, cancers, diabetes, Parkinson's disease, osteoporosis, myocardial
 CC infarction, ulcers, asthma, allergies, angina pectoris, renal disease,
 CC depression, schizophrenia, anorexia, obesity, Kallman's syndrome,
 CC hypothalamic disorders, idiopathic hormone deficiency (e.g. gigantism),
 CC migraine, pain, lung diseases, burns, sleep disorders, jet lag,
 CC Huntington's disease and many other diseases and disorders given in the
 CC specification. The present sequence is the human HFGAN72X receptor being
 CC the product of a splice variant of HFGAN72
 XX
 SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 4; Length 425;
 Best Local Similarity 100.0%; Pred. No. 6.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLF SVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSLPELANRTRLF SVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDL EQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDL EQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363
  
```

RESULT 10

AAB67079

ID AAB67079 standard; protein; 425 AA.

XX

AC AAB67079;

XX

DT 10-APR-2001 (first entry)

XX

DE Human HFGAN72 receptor SEQ ID NO: 13.

XX

KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;

KW truncation mutant; ligand; neurodegenerative disorder; pain;

KW eating disorder; behaviour disorder; mood disorder.

XX

OS Homo sapiens.

XX

PN WO200100787-A2.

XX

PD 04-JAN-2001.

XX

PF 22-JUN-2000; 2000WO-US017251.

XX

PR 25-JUN-1999; 99US-0141156P.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR WPI; 2001-071483/08.
XX
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.
XX
PS Claim 8; Fig 7; 101pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 4; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
      |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
      |||
Db    121 VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      |||
Db    181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLLVFALCYLPISVLNVLKRVEFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      |||
Db    301 MVLLVFALCYLPISVLNVLKRVEFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
      |||
Db    361 LSG 363

```

RESULT 11

AAG78345

ID AAG78345 standard; protein; 425 AA.

XX

AC AAG78345;

XX

DT 22-JAN-2002 (first entry)

XX

DE Human HFGAN72X G coupled receptor polypeptide.

XX

KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor.

XX

OS Homo sapiens.

XX

PN EP1154019-A2.

XX

PD 14-NOV-2001.

XX

PF 27-OCT-1997; 2001EP-00203008.

XX

PR 30-APR-1997; 97US-00846704.

PR 27-OCT-1997; 97EP-00308563.

XX

PA (SMIK) SMITHKLINE BEECHAM CORP.

XX

PI Bergsma DJ, Ellis CE;

XX

DR WPI; 2002-012659/02.

DR N-PSDB; AAI64172.

XX

PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.

XX

PS Claim 11; Page 7-8; 24pp; English.

XX

CC The present sequence is that of a human HFGAN72X polypeptide encoded by a
CC cDNA shown in AAI64172. The specification describes a newly isolated
CC polynucleotide encoding a HFGAN72X G coupled receptor polypeptide. The
CC protein of the invention has antibacterial, fungicide, virucide,
CC protozoacide, anti-HIV, cardiant, analgesic, cytostatic, nootropic,
CC antiparkinsonian, antiulcer, antiasthmatic, tranquiliser, neuroleptic,
CC antidepressant, anticonvulsant and osteopathic activities. HFGAN72X
CC polynucleotides (PNs) are used to express HFGAN72X in vivo, to treat
CC diseases requiring increased activity or expression of HFGAN72X; for
CC recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X

CC PNs are used to identify (ant)agonists of HFGAN72X, useful
 CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
 CC polypeptides that compete with ligands for binding to HFGAN72X proteins
 CC are also useful therapeutically and diagnostically. HFGAN72X-related
 CC diseases include infections (bacterial, viral, fungal or protozoal,
 CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
 CC disease; acute heart failure; hypotension; hypertension; urinary
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
 CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
 CC manic depression; delirium; dementia; severe mental retardation and
 CC dyskinesias
 XX
 SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 5; Length 425;
 Best Local Similarity 100.0%; Pred. No. 6.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSR	EPSPVP	PDYED	EFRLYLWRDYL	YPKQYEWV	LIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSR	EPSPVP	PDYED	EFRLYLWRDYL	YPKQYEWV	LIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNH	MRTVTNYFIVN	LSLADVLVTAIC	LPASLLVDIT	ESWLFGHALCK	120	
Db	61	LVGNTLVCLAVWRNH	MRTVTNYFIVN	LSLADVLVTAIC	LPASLLVDIT	ESWLFGHALCK	120	
Qy	121	VIPYLQAVSVSAVL	TLSFIALDRWYA	ICHPLLEFKST	ARRARGSILGI	WAVSLAIMVPQA	180	
Db	121	VIPYLQAVSVSAVL	TLSFIALDRWYA	ICHPLLEFKST	ARRARGSILGI	WAVSLAIMVPQA	180	
Qy	181	AVMECSSVLPELAN	RTRLFSVCDER	WADDLYPKIYH	SCFFIVTYLAP	LGLMAMAYFQIFR	240	
Db	181	AVMECSSVLPELAN	RTRLFSVCDER	WADDLYPKIYH	SCFFIVTYLAP	LGLMAMAYFQIFR	240	
Qy	241	KLWGRQIPGTT	SALVRNWKRP	SDQLGDL	EQGLSGEPQPR	GRAFLAEVKQMR	RARRKTAKML 300	
Db	241	KLWGRQIPGTT	SALVRNWKRP	SDQLGDL	EQGLSGEPQPR	GRAFLAEVKQMR	RARRKTAKML 300	
Qy	301	MVLLVFALCYLP	ISVLNVLKR	VFGMFRQASD	REAVYACFTF	SHWL	VYANSAANPIIYNF 360	
Db	301	MVLLVFALCYLP	ISVLNVLKR	VFGMFRQASD	REAVYACFTF	SHWL	VYANSAANPIIYNF 360	
Qy	361	LSG	363					
Db	361	LSG	363					

RESULT 12

ABP81941

ID ABP81941 standard; protein; 425 AA.

XX

AC ABP81941;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human orexin receptor 1 protein SEQ ID NO:368.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;
KW ulcer.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

XX

PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.

XX

PI Burmer GC, Roush CL, Brown JP;

XX

DR WPI; 2003-046718/04.

DR N-PSDB; ABZ42789.

XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

XX

PS Disclosure; Fig 1; 523pp; English.

XX

CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or

CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 6; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVQA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVQA 180

Qy    181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy     361 LSG 363
      |||
Db     361 LSG 363
```

RESULT 13

ABG75058

ID ABG75058 standard; protein; 425 AA.

XX

AC ABG75058;

XX

DT 12-FEB-2004 (first entry)

XX

DE Human orexin receptor 1 protein.

XX

KW Energy homeostasis; mouse; metabolism; triglyceride; metabolic disease;
KW gene therapy; anorectic; immunomodulator; antidiabetic; hypotensive;
KW cardiant; osteopathic; antilipemic.

XX

OS Homo sapiens.

XX

PN WO2003075945-A2.

XX
PD 18-SEP-2003.
XX
PF 14-MAR-2003; 2003WO-EP002714.
XX
PR 14-MAR-2002; 2002EP-00005882.
PR 15-MAR-2002; 2002EP-00006012.
PR 20-MAR-2002; 2002EP-00006271.
PR 25-MAR-2002; 2002EP-00006810.
XX
PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
XX
PI Eulenberg K, Steuernagel A, Haeder T, Broenner G;
XX
DR WPI; 2003-748334/70.
DR N-PSDB; ACH00818.
XX
PT New pharmaceutical composition comprising a nucleic acid molecule
PT encoding proteins regulating the energy homeostasis and metabolism of
PT triglycerides useful for detecting or preventing metabolic diseases, e.g.
PT obesity.
XX
PS Claim 3; Fig 7G; 140pp; English.
XX
CC The present invention relates to pharmaceutical compositions comprising
CC the coding sequences shown in ACH00815-ACH00827, or their encoded
CC proteins (shown in ABG75054, ABG75056-ABG75067). These are proteins
CC involved in the metabolism of triglycerides and in energy homeostasis,
CC and their coding sequences. The composition is useful for the manufacture
CC of an agent for detecting, verifying, treating, alleviating or preventing
CC disorders, including metabolic diseases such as obesity and other body-
CC weight regulation disorders as well as related disorders such as
CC metabolic syndrome, eating disorder, cachexia, diabetes mellitus,
CC hypertension, coronary heart disease, hypercholesterolaemia,
CC dyslipidaemia, osteoarthritis or gallstones, in cells, cell masses,
CC organs or subjects. The coding sequences can be used in the production of
CC transgenic animals which under- or over-produce the gene of interest. The
CC present sequence is a protein of the invention
XX
SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 7; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-187;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 14

ADK52564

ID ADK52564 standard; protein; 425 AA.

XX

AC ADK52564;

XX

DT 06-MAY-2004 (first entry)

XX

DE Hematological disorder associated Gene ID 14393 encoded protein.

XX

KW cytostatic; antianemic; antisickling; virucide; hemostatic; nephrotropic;

KW cytostatic; thrombolytic; antiparasitic; gene therapy;

KW hematologic disorder; cancer; Sickle Cell Anemia;

KW Infectious Mononucleosis; Leukemia; Polycythemia Vera; Lymphoma;

KW Retinoblastoma; Hemophilia; Thrombosis; Herpes; Thalassemia;

KW transfusion reaction; Erythroblastosis; mechanical trauma;

KW micro-angiopathic hemolytic anemia; parasite infection.

XX

OS Homo sapiens.

XX

PN WO2003065871-A2.

XX

PD 14-AUG-2003.

XX

PF 28-JAN-2003; 2003WO-US002484.

XX

PR 04-FEB-2002; 2002US-0354333P.

PR 28-FEB-2002; 2002US-0360258P.

PR 15-MAR-2002; 2002US-0364476P.

PR 26-APR-2002; 2002US-0375626P.

PR 06-JUN-2002; 2002US-0386494P.

PR 24-JUN-2002; 2002US-0390965P.

PR 28-JUN-2002; 2002US-0392480P.

PR 03-JUL-2002; 2002US-0394128P.

PR 31-JUL-2002; 2002US-0399783P.

PR 13-AUG-2002; 2002US-0403221P.

PR 30-AUG-2002; 2002US-0407045P.

PR 25-NOV-2002; 2002US-0429048P.

XX

PA (MILL-) MILLENNIUM PHARM INC.

XX
 PI Carroll JM, Healy A, Weich NS, Kelly LM;
 XX
 DR WPI; 2003-731464/69.
 DR N-PSDB; ADK52563.
 XX
 PT Identifying a compound capable of treating a hematologic disorder (e.g.
 PT anemia or leukemia) comprises assaying the ability of the compound to
 PT modulate the expression or activity of e.g. 131,148, 199 or 12303
 PT polypeptide or nucleic acid.
 XX
 PS Disclosure; SEQ ID NO 22; 232pp; English.
 XX
 CC The invention relates to a method of identifying a compound capable of
 CC treating a hematologic disorder comprises assaying the ability of the
 CC compound to modulate 131,148, 199, 12303, 13906, 15513, 17822, 302, 5677,
 CC 194, 14393, 28059, 7366, 12212, 1981, 261, 12416, 270, 1410, 137, 1871,
 CC 13051, 1847, 1849, 15402, 340, 10217, 837, 1761, 8990 or 13249 nucleic
 CC acid expression or polypeptide activity, thus, identifying a compound
 CC capable of treating a hematologic disorder. The methods are useful in
 CC diagnosing, preventing and treating hematological disorders, such as
 CC cancer, Sickie Cell Anemia, Infectious Mononucleosis, Leukemia,
 CC Polycythemia Vera, Lymphoma, Retinoblastoma, Hemophilia, disorders
 CC associated with an increased risk of Thrombosis, Herpes, Thalassemia,
 CC antibody-mediated disorders such as transfusion reactions and
 CC Erythroblastosis, mechanical trauma to red blood cells such as micro-
 CC angiopathic hemolytic anemias, infections by parasites or chemical
 CC injuries. The methods may also be used for identifying compounds that
 CC modulate hematological disorders. This sequence corresponds to the
 CC protein encoded by one of the genes modulated by the compounds.
 XX
 SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 7; Length 425;
 Best Local Similarity 100.0%; Pred. No. 6.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSREPSVPVPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 15

ADL22443

ID ADL22443 standard; protein; 425 AA.

XX

AC ADL22443;

XX

DT 20-MAY-2004 (first entry)

XX

DE Human orexin 1 receptor variant protein.

XX

KW polydipsia; single nucleotide polymorphism; SNP; orexin 1 receptor gene;

KW schizophrenia; human; mutant; mutein.

XX

OS Homo sapiens.

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 408

FT /note= "The wild-type residue of Ile is substituted with
 FT Val at this position following a single nucleotide
 FT polymorphism in the encoding gene"

XX

PN JP2004041055-A.

XX

PD 12-FEB-2004.

XX

PF 10-JUL-2002; 2002JP-00201575.

XX

PR 10-JUL-2002; 2002JP-00201575.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI; 2004-208085/20.

DR N-PSDB; ADL22427.

XX

PT Estimating whether subject has factor of polydipsia, comprises

PT determining single nucleotide polymorphism in orexin 1 receptor gene

PT and/or at least one polymorphism in linkage disequilibrium.

XX

PS Claim 11; Page; 31pp; Japanese.

XX

CC The invention relates to a novel method for estimating whether a subject
 CC has a factor of polydipsia. The method comprises determining a single
 CC nucleotide polymorphism (SNP) at position 1222 of a fully defined orexin
 CC 1 receptor gene sequence of 1411 nucleotides, as given in the
 CC specification, and/or at least one polymorphism in the linkage
 CC disequilibrium from a biological sample obtained from a subject. A
 CC polynucleotide of at least 10 contiguous bases comprising the SNP at

CC position 1222 is useful for estimating whether a subject comprises a
 CC factor of polydipsia. A polypeptide having a polymorphic variation in the
 CC human orexin 1 receptor or its fragment, or a transformed cell which
 CC expresses the polypeptide is useful for the screening of a compound that
 CC controls the function of the human orexin 1 receptor. The method allows
 CC detection of polydipsia, which is a serious symptom of schizophrenia and
 CC therefore useful in the selection of a treatment for preventing the
 CC symptom. This sequence represents the variant protein following the SNP
 CC at position 1222 of the 1411 nt human orexin 1 receptor gene of the
 CC invention. Note: This sequence is not shown in the specification. It has
 CC been created from the protein of SEQ ID No 2 and information provided in
 CC claim 11 of the specification.

XX

SQ Sequence 425 AA;

Query Match 97.7%; Score 1903; DB 8; Length 425;
 Best Local Similarity 100.0%; Pred. No. 6.3e-187;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGPVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA	180
Qy	181	AVMECSSLVPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSLVPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

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 Job time : 90.6501 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:43:25 ; Search time 22.6518 Seconds
(without alignments)
1089.110 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPIIYNFLSGCKEKSILVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

8							
Result	Query						
No.	Score	Match	Length	DB	ID	Description	
1	1947	100.0	377	5	PCT-US95-05616-6	Sequence 6, Appli	
2	1944	99.8	372	4	US-08-462-509B-6	Sequence 6, Appli	
3	1943	99.8	389	2	US-08-846-705-2	Sequence 2, Appli	
4	1943	99.8	389	4	US-09-211-823C-23	Sequence 23, Appl	
5	1903	97.7	369	4	US-08-462-509B-4	Sequence 4, Appli	
6	1903	97.7	369	5	PCT-US95-05616-4	Sequence 4, Appli	
7	1903	97.7	402	4	US-08-462-509B-2	Sequence 2, Appli	
8	1903	97.7	402	5	PCT-US95-05616-2	Sequence 2, Appli	
9	1903	97.7	425	3	US-08-846-704-2	Sequence 2, Appli	
10	1903	97.7	425	4	US-09-211-823C-22	Sequence 22, Appl	
11	1897	97.4	402	3	US-08-846-704-4	Sequence 4, Appli	

12	1897	97.4	425	3	US-09-479-128-2	Sequence 2, Appli
13	1341.5	68.9	444	4	US-09-426-290-2	Sequence 2, Appli
14	1340.5	68.8	444	3	US-09-119-788-2	Sequence 2, Appli
15	1307	67.1	263	3	US-08-513-974B-54	Sequence 54, Appl
16	1307	67.1	263	3	US-08-513-974B-376	Sequence 376, App
17	1307	67.1	263	4	US-09-461-436B-54	Sequence 54, Appl
18	485.5	24.9	430	3	US-09-255-368-8	Sequence 8, Appli
19	485.5	24.9	430	4	US-09-405-558-8	Sequence 8, Appli
20	480.5	24.7	432	3	US-09-255-368-2	Sequence 2, Appli
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22	476.5	24.5	420	3	US-09-255-368-6	Sequence 6, Appli
23	476.5	24.5	420	4	US-09-405-558-6	Sequence 6, Appli
24	472	24.2	417	4	US-09-405-558-44	Sequence 44, Appl
25	417	21.4	370	3	US-09-172-353-2	Sequence 2, Appli
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27	417	21.4	370	4	US-09-799-955-2	Sequence 2, Appli
28	417	21.4	370	4	US-09-799-955-3	Sequence 3, Appli
29	413.5	21.2	370	3	US-09-172-353-7	Sequence 7, Appli
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31	413	21.2	370	3	US-08-513-974B-26	Sequence 26, Appl
32	413	21.2	370	3	US-08-513-974B-323	Sequence 323, App
33	413	21.2	370	3	US-09-172-353-5	Sequence 5, Appli
34	413	21.2	370	3	US-08-776-971-21	Sequence 21, Appl
35	413	21.2	370	3	US-08-776-971-104	Sequence 104, App
36	413	21.2	370	4	US-09-799-955-5	Sequence 5, Appli
37	413	21.2	370	4	US-09-461-436B-26	Sequence 26, Appl
38	413	21.2	370	4	US-09-576-290-21	Sequence 21, Appl
39	413	21.2	370	4	US-09-576-290-104	Sequence 104, App
40	406.5	20.9	370	3	US-08-776-971-140	Sequence 140, App
41	406.5	20.9	370	4	US-09-576-290-140	Sequence 140, App
42	404.5	20.8	381	2	US-08-687-355A-4	Sequence 4, Appli
43	404.5	20.8	381	4	US-09-407-367-4	Sequence 4, Appli
44	404	20.7	381	1	US-08-192-288-2	Sequence 2, Appli
45	404	20.7	381	2	US-08-687-355A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1

PCT-US95-05616-6

; Sequence 6, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

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;   OPERATING SYSTEM:  MS-DOS
;   SOFTWARE:  WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US95/05616
;   FILING DATE:  concurrently
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  FERRARO, GREGORY D.
;   REGISTRATION NUMBER:  36,134
;   REFERENCE/DOCKET NUMBER:  325800-268
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-994-1700
;   TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  377 BASE PAIRS
;   TYPE:  AMINO ACID
;   STRANDEDNESS:  SINGLE
;   TOPOLOGY:  LINEAR
;   MOLECULE TYPE:  cDNA
PCT-US95-05616-6

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Query Match          100.0%;  Score 1947;  DB 5;  Length 377;
Best Local Similarity 100.0%;  Pred. No. 3.3e-178;
Matches 372;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
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Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGCKEKS LVLS 372
      |||||||||
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RESULT 2
US-08-462-509B-6

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; Sequence 6, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Human Genome Sciences, Inc.
;     STREET: 9410 Key West Avenue
;     CITY: Rockville
;     STATE: MD
;     COUNTRY: USA
;     ZIP: 20850
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/462,509B
;     FILING DATE: 05-JUN-1995
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: WO PCT/US95/05616
;     FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Wales, Michele M.
;     REGISTRATION NUMBER: 43,975
;     REFERENCE/DOCKET NUMBER: PF168P1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 301-309-8504
;     TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 6:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 372 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-462-509B-6

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```

Query Match          99.8%; Score 1944; DB 4; Length 372;
Best Local Similarity 99.7%; Pred. No. 6.3e-178;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSRFPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||:||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGPVPPGSRFPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

```

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

QY      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

QY      301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVIYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 MVVLLVFALCYLPISVLNVLKRIVFGMFRQASDREAVYACFTFSHWLVIYANSAANPIIYNF 360

QY      361 LSGCKEKSLLVLS 372
      ||||||||||||
Db      361 LSGCKEKSLLVLS 372

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RESULT 3

US-08-846-705-2

; Sequence 2, Application US/08846705

; Patent No. 5935814

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,705

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0701

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 389 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-846-705-2

Query Match 99.8%; Score 1943; DB 2; Length 389;
Best Local Similarity 99.7%; Pred. No. 8.4e-178;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MCVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MCVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGCKEKSILVLS 372
          |||
Db    361 LSGCKEKSILVLS 372
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RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Patent No. 6664229

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-23

Query Match 99.8%; Score 1943; DB 4; Length 389;
Best Local Similarity 99.7%; Pred. No. 8.4e-178;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
|
Db 1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
|
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
|
Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy 181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|
Db 181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|
Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|
Db 301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSGCKEKSLLVS 372
|
Db 361 LSGCKEKSLLVS 372

RESULT 5

US-08-462-509B-4

; Sequence 4, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD
; COUNTRY: USA

```

;      ZIP: 20850
;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: IBM PC compatible
;      OPERATING SYSTEM: PC-DOS/MS-DOS
;      SOFTWARE: PatentIn Release #1.0, Version #1.30
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/08/462,509B
;      FILING DATE: 05-JUN-1995
;      CLASSIFICATION: 435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: WO PCT/US95/05616
;      FILING DATE: 05-MAY-1995
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Wales, Michele M.
;      REGISTRATION NUMBER: 43,975
;      REFERENCE/DOCKET NUMBER: PF168P1
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 301-309-8504
;      TELEFAX: 301-309-8439
;      INFORMATION FOR SEQ ID NO: 4:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 369 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
US-08-462-509B-4

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```

Query Match          97.7%; Score 1903; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 MEPSATPGAQMGVPPGSRPEPSVPPDYEDFLRYLWRDYLPKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSRPEPSVPPDYEDFLRYLWRDYLPKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363

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Db 361 LSG 363

RESULT 6
PCT-US95-05616-4
; Sequence 4, Application PC/TUS9505616
; GENERAL INFORMATION:
; APPLICANT: LI, ET AL.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05616
; FILING DATE: concurrently
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 369 BASE PAIRS
; TYPE: AMINO ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA
PCT-US95-05616-4

Query Match 97.7%; Score 1903; DB 5; Length 369;
Best Local Similarity 100.0%; Pred. No. 5.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEQYEWVLIAAYVAVFVVA 60

QY     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

QY    121 VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
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```

Db      121 VIPYLQAVSVSAVLTLTSLFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPGA 180
Qy      181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Db      181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
Qy      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Qy      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSG 363
Db      361 LSG 363

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RESULT 7

US-08-462-509B-2

; Sequence 2, Application US/08462509B

; Patent No. 6410701

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/462,509B

; FILING DATE: 05-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: WO PCT/US95/05616

; FILING DATE: 05-MAY-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 402 amino acids

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-462-509B-2

Query Match 97.7%; Score 1903; DB 4; Length 402;
Best Local Similarity 100.0%; Pred. No. 5.9e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGI WAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MCVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MCVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy     361 LSG 363
        |||
Db     361 LSG 363
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RESULT 8

PCT-US95-05616-2

; Sequence 2, Application PC/TUS9505616

; GENERAL INFORMATION:

; APPLICANT: LI, ET AL.

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,

; ADDRESSEE: CECCHI, STEWART & OLSTEIN

; STREET: 6 BECKER FARM ROAD

; CITY: ROSELAND

; STATE: NEW JERSEY

; COUNTRY: USA

; ZIP: 07068

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 INCH DISKETTE

; COMPUTER: IBM PS/2

; OPERATING SYSTEM: MS-DOS

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;   SOFTWARE:  WORD PERFECT 5.1
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US95/05616
;   FILING DATE:  concurrently
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  FERRARO, GREGORY D.
;   REGISTRATION NUMBER:  36,134
;   REFERENCE/DOCKET NUMBER:  325800-268
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  201-994-1700
;   TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  2:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  402 AMINO ACIDS
;   TYPE:  AMINO ACID
;   STRANDEDNESS:
;   TOPOLOGY:  LINEAR
;   MOLECULE TYPE:  PROTEIN
PCT-US95-05616-2

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```

Query Match          97.7%;  Score 1903;  DB 5;  Length 402;
Best Local Similarity 100.0%;  Pred. No. 5.9e-174;
Matches 363;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
        |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180
        |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db    241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db    301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363

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RESULT 9
US-08-846-704-2
; Sequence 2, Application US/08846704

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; Patent No. 6020157
; GENERAL INFORMATION:
;   APPLICANT: BERGSMA, DERK J.
;   APPLICANT: ELLIS, CATHERINE E.
;   TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED
;   NUMBER OF SEQUENCES: 4
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: RATNER & PRESTIA
;     STREET: P.O. BOX 980
;     CITY: VALLEY FORGE
;     STATE: PA
;     COUNTRY: USA
;     ZIP: 19482
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Diskette
;     COMPUTER: IBM Compatible
;     OPERATING SYSTEM: DOS
;     SOFTWARE: FastSEQ for Windows Version 2.0
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/846,704
;     FILING DATE: 30-APR-1997
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:
;     FILING DATE:
;   ATTORNEY/AGENT INFORMATION:
;     NAME: PRESTIA, PAUL F
;     REGISTRATION NUMBER: 23,031
;     REFERENCE/DOCKET NUMBER: GH-70002
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: 610-407-0700
;     TELEFAX: 610-407-0701
;     TELEX: 846169
;   INFORMATION FOR SEQ ID NO: 2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH: 425 amino acids
;       TYPE: amino acid
;       STRANDEDNESS: single
;       TOPOLOGY: linear
;     MOLECULE TYPE: protein
US-08-846-704-2

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Query Match          97.7%; Score 1903; DB 3; Length 425;
Best Local Similarity 100.0%; Pred. No. 6.3e-174;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180

```

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTTTALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 10

US-09-211-823C-22

; Sequence 22, Application US/09211823C

; Patent No. 6664229

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 22

; LENGTH: 425

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-211-823C-22

Query Match 97.7%; Score 1903; DB 4; Length 425;

Best Local Similarity 100.0%; Pred. No. 6.3e-174;

Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60
 |||

Db 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGRHALCK 120

Qy      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
      |||
Db      361 LSG 363

```

RESULT 11

US-08-846-704-4

; Sequence 4, Application US/08846704

; Patent No. 6020157

; GENERAL INFORMATION:

; APPLICANT: BERGSMA, DERK J.

; APPLICANT: ELLIS, CATHERINE E.

; TITLE OF INVENTION: NOVEL G-PROTEIN COUPLED

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: RATNER & PRESTIA

; STREET: P.O. BOX 980

; CITY: VALLEY FORGE

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/846,704

; FILING DATE: 30-APR-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: PRESTIA, PAUL F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GH-70002

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700
 ; TELEFAX: 610-407-0701
 ; TELEX: 846169
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 402 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-846-704-4

Query Match 97.4%; Score 1897; DB 3; Length 402;
 Best Local Similarity 99.7%; Pred. No. 2.2e-173;
 Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA	60
Db	1	MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA	60
Qy	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF	120
Db	61	LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF	120
Qy	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA	180
Qy	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Db	181	AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR	240
Qy	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML	300
Db	241	KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML	300
Qy	301	MVLLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Db	301	MVLLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF	360
Qy	361	LSG	363
Db	361	LSG	363

RESULT 12
 US-09-479-128-2
 ; Sequence 2, Application US/09479128
 ; Patent No. 6319710
 ; GENERAL INFORMATION:
 ; APPLICANT: Berglind Ran Olafsdottir
 ; APPLICANT: Jeffrey Gulcher
 ; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
 ; FILE REFERENCE: 2345.1005-001
 ; CURRENT APPLICATION NUMBER: US/09/479,128
 ; CURRENT FILING DATE: 2000-01-07
 ; PRIOR APPLICATION NUMBER: US 09/379,083

; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-479-128-2

Query Match 97.4%; Score 1897; DB 3; Length 425;
Best Local Similarity 99.7%; Pred. No. 2.4e-173;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
|
Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
|
Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPPA 180
|
Db 121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPPA 180

Qy 181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
|
Db 181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
|
Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
|
Db 301 MVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
|
Db 361 LSG 363

RESULT 13

US-09-426-290-2

; Sequence 2, Application US/09426290
; Patent No. 6410712
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.2001-000
; CURRENT APPLICATION NUMBER: US/09/426,290
; CURRENT FILING DATE: 1999-10-25
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 444

; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-426-290-2

Query Match 68.9%; Score 1341.5; DB 4; Length 444;
Best Local Similarity 71.4%; Pred. No. 3.7e-120;
Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

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Qy      17 SREPSVPPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVVRNH 75
          ::|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:| ||:| |
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135
          ||||| ||||| |||||:| |||||:| || : ||||| |||||:| |
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQAAMVMECSSLPELANR 195
          ||| ||||| |||||:| |||||:| || : || || ||:| || |||||:| | ||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

Qy     196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
          | ||:| |||| | :|||:| || |:| ||||:| || :| ||||| |||||:| :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCIMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
          | || | || | ||| | ||:|:| |||||:| ||||| |
Db     264 RKWK-----PLQPVSQPRGPQPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312

Qy     307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
          ||:| |||||:| ||||| || || || ||||| ||||| ||||| |||||
Db     313 FAICYLPISILNVLKRVFGMFAHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369
```

RESULT 14

US-09-119-788-2

; Sequence 2, Application US/09119788

; Patent No. 6166193

; GENERAL INFORMATION:

; APPLICANT: Yanagisawa, Masashi

; TITLE OF INVENTION: CDNA CLONE MY1 THAT ENCODES

; TITLE OF INVENTION: A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SmithKline Beecham Corporation

; STREET: 709 Swedeland Road

; CITY: King of Prussia

; STATE: PA

; COUNTRY: United States of America

; ZIP: 19406

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/119,788

; FILING DATE: 21-JUL-1998

```

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/053,790
; FILING DATE: 25-JUL-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: King, William T
; REGISTRATION NUMBER: 30,954
; REFERENCE/DOCKET NUMBER: GH50029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5515
; TELEFAX: 610-270-5090
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-119-788-2

```

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Query Match          68.8%; Score 1340.5; DB 3; Length 444;
Best Local Similarity 71.4%; Pred. No. 4.6e-120;
Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

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Qy      17 SREPSVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
      :||| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCKVIPYLQAVSVSVAVL 135
      |||||:|:|:| |||||:| || :||| |||||:| ||||:|
Db      84 HMRTVTNYFIVNLSLADVLTITCLPATLVVDITETWFFGQSLCKVIPYLTQTVSVSVSVL 143

Qy      136 TLSFIALDRWYAICHPLLFKSTARRARGSSILGIWAVSLAIMVPQAAMECSSLPELANR 195
      ||| |||||:|:|:| ||| ||: || || ||:| || ||||:| |||:
Db      144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVIIWIVSCIIMIPQAIVMECSTVFPLANK 203

Qy      196 TRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSAV 255
      | ||:| |||| :||:| |||:|:| || || :|| ||||| |||||:| :
Db      204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy      256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVVLLV 306
      | || | ||| | ||:|:| |||||:| |||||
Db      264 RKWK-----PLQPVSQPRGPGQPTKSRMGAVAAEIKQIRARRKTARMLMVVLLV 312

Qy      307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
      ||:| |||||:| ||||| ||| || ||||| ||||| |||||
Db      313 FAICYLPISILNVLKRVFGMFAHTEDRETVEYAWFTFSHWLVYANSAANPIIYNFLSG 369

```

RESULT 15

US-08-513-974B-54

; Sequence 54, Application US/08513974B

; Patent No. 6114139

; GENERAL INFORMATION:

; APPLICANT: Hinuma, Shuji

; APPLICANT: Hosoya, Masaki

; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
; TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
; NUMBER OF SEQUENCES: 380
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/513,974B
; FILING DATE: 14-SEP-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-093989
; FILING DATE: 19-AUG-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-057186
; FILING DATE: 16-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 7-007177
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-326611
; FILING DATE: 28-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-270017
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236357
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-236356
; FILING DATE: 30-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189274
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189273
; FILING DATE: 11-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:

```

;      NAME:  Resnick, David S.
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  45753
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      INFORMATION FOR SEQ ID NO:  54:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  263 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
US-08-513-974B-54

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Query Match          67.1%;  Score 1307;  DB 3;  Length 263;
Best Local Similarity 96.2%;  Pred. No. 3.8e-117;
Matches 253;  Conservative 2;  Mismatches 8;  Indels 0;  Gaps 0;

```

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Qy      91 ADVLVTAICLPASLLVDITESWLFQHALCKVIPYLAQAVSVSVAVLTLSFIALDRWYAICH 150
          |||
Db      1  ADVLVTAICLPASLLVDITESWLFQHALCKVIPYLAQAVSVSVVLTLSIALDRWYAICH 60

Qy     151 PLLFKSTARRARGSI LGIWA VSLAIMVPQA AVM ECSSVLPELANRTR LFSVCDERWADDL 210
          |||
Db      61 PLLFKSTARRARGSI LGIWA VSLAVMVPQA AVM ECSSVLPELANRTR LLSVCDERWADDL 120

Qy     211 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQ 270
          |||
Db     121 YPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLDDQGG 180

Qy     271 GLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQGMFRQA 330
          |||
Db     181 GLSSEPQPRARAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQGMFRQA 240

Qy     331 SDREAVYACFTTFSHWLVIYANSAA 353
          |||
Db     241 SDREAIYACFTTFSHWLVIYANSAA 263

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Search completed: October 14, 2004, 10:58:13
Job time : 23.6518 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:42:40 ; Search time 19.7804 Seconds
(without alignments)
1809.496 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMVGVPGRSREP.....ANPIIYNFLSGCKEKSILVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	422.5	21.7	449	2	A41738	neuropeptide Y rec
2	413.5	21.2	370	1	I52315	G protein-coupled
3	404	20.7	381	2	I39187	neuropeptide Y/pep
4	391	20.1	427	2	S50150	gastric CCK-A rece
5	383.5	19.7	465	1	JQ1517	neurokinin 3 recep
6	382.5	19.6	519	2	S17783	tachykinin recepto
7	382	19.6	452	2	A34916	neurokinin 3 recep
8	379.5	19.5	452	2	JC2459	gastrin/cholecysto
9	379	19.5	584	2	JC7809	sulfakinin recepto
10	376.5	19.3	450	2	JQ1614	gastrin receptor -
11	376	19.3	385	2	S55524	neurokinin 3 recep
12	373.5	19.2	428	2	JN0692	cholecystokinin ty
13	373.5	19.2	452	2	A46195	cholecystokinin B

14	373	19.2	447	2	A47430	gastrin/cholecysto
15	371.5	19.1	423	2	B40470	glucocorticoid-ind
16	369.5	19.0	430	2	I51898	cholecystokinin A
17	368	18.9	402	2	I56595	neurokinin 2 recep
18	368	18.9	440	2	A44081	kappa-type opioid
19	367	18.8	349	2	I59336	galanin receptor 1
20	367	18.8	366	2	S71152	neuropeptide Y/pep
21	365	18.7	453	2	S32817	gastrin receptor -
22	362.5	18.6	407	2	S23510	neurokinin 1 recep
23	361	18.5	384	1	S00516	neurokinin 2 recep
24	361	18.5	444	2	A42685	cholecystokinin re
25	360	18.5	398	1	JQ1059	neurokinin 2 recep
26	359.5	18.5	407	1	JQ1274	neurokinin 1 recep
27	359.5	18.5	480	2	I53053	beta 1 adrenergic
28	359	18.4	423	2	JC7677	allatostatin recep
29	358.5	18.4	407	2	A34357	neurokinin 1 recep
30	358	18.4	477	1	QRHUB1	beta-1-adrenergic
31	357.5	18.4	407	2	S20304	neurokinin 1 recep
32	355.5	18.3	387	2	JC5949	galanin receptor 2
33	355	18.2	384	2	I57957	neurokinin 2 recep
34	354	18.2	394	2	JC7209	galanin receptor -
35	353.5	18.2	443	2	D40470	glucocorticoid-ind
36	353	18.1	390	2	A36737	neurokinin 2 recep
37	351	18.0	390	2	B41007	bombesin receptor,
38	350	18.0	483	2	A25896	beta-adrenergic re
39	348.5	17.9	436	2	JC5599	cholecystokinin-A
40	345.5	17.7	466	2	S36794	beta-1-adrenergic
41	345.5	17.7	504	2	A41783	tachykinin recepto
42	344	17.7	464	2	S12591	beta-1-adrenergic
43	343	17.6	375	2	S63685	neuropeptide Y rec
44	342	17.6	375	2	I39182	neuropeptide Y/pep
45	342	17.6	384	2	S20303	neurokinin 2 recep

ALIGNMENTS

RESULT 1

A41738

neuropeptide Y receptor - fruit fly (*Drosophila melanogaster*)

N;Alternate names: G protein-coupled receptor PR4

C;Species: *Drosophila melanogaster*

C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004

C;Accession: A41738

R;Li, X.J.; Wu, Y.N.; North, R.A.; Forte, M.

J. Biol. Chem. 267, 9-12, 1992.

A;Title: Cloning, functional expression, and developmental regulation of a neuropeptide Y receptor from *Drosophila melanogaster*.

A;Reference number: A41738; MUID:92112730; PMID:1370455

A;Accession: A41738

A;Molecule type: mRNA

A;Residues: 1-449 <LIA>

A;Cross-references: UNIPROT:P25931; GB:M81490; NID:g157996; PIDN:AAA28727.1; PID:g157997

C;Genetics:

A;Gene: FlyBase:NepYr

A;Cross-references: FlyBase:FBgn0004842

C;Superfamily: neurokinin 1 receptor

C;Keywords: appetite; G protein-coupled receptor; transmembrane protein

Query Match 21.7%; Score 422.5; DB 2; Length 449;
Best Local Similarity 29.7%; Pred. No. 3.5e-28;
Matches 102; Conservative 61; Mismatches 128; Indels 53; Gaps 8;

```
Qy      26 DYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHMRTVTNYFI 85
      ||:  |  |  ::  ::  |:  ::  ||:  ||  |  |  |||||
Db      75 DYD-----LLSEDMWSSAYFKIIVYMLYIPIFIFALINGTVCYIVYSTPRMRTVTNYFI 129

Qy      86 VNLSLADVLVTAICLPASLL-VDITESWLFQHALCKVIPYLQAVSVSAVLTLSFIALDR 144
      :||:  |:|:  |  |:|  :  :  |  ||  ||  :  |  ||||  |:  ||  |:|:
Db     130 ASLAIGDILMSFFCEPSSFISLFILNYWPFGLALCHFVNYSQAVSVLVSAITLVAISIDR 189

Qy     145 WYAICHPLLKSTARRARGSI LGIWA VSLAIMVPQAAVMECSSVLPELANRTRLFSVCDE 204
      :  ||  ||  :  |  |  |  |  |:|  ::||  :|  |  :  :  :  :  |
Db     190 YIAIMWPLKPRITKRYATFIIAGVWFIALATALPIPIVSGLDIPMPWHTKCEKY-ICRE 248

Qy     205 RWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTALVRNWKRPDSQ 264
      |  |  |  |  :  ::  |||:  |  :|  ::|  ::  ||  :  ||
Db     249 MWPSRSQEYYYTSLSFALQFVVLPLGVLIIFTYARITIRVWAKRPPGEA-----ETNRDQ 301

Qy     265 LGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVF 324
      :  |:|  ||  ||:  |:|  ||  |:|  ::|  :|
Db     302 -----RMARSKRKMVKMMLTVVIVFTCCWLPFNILQLL---- 334

Qy     325 GMFRQASDREAV-----YACFTFSHWLVYANSAANPIIYNFLS 362
      :|  |  |  |  |  ||  ||  ::  ||||  ::
Db     335 -----LNDEEFAHWDPLPYVWFAF-HWLAMSHCCYNPIIYCYMN 372
```

RESULT 2

I52315

G protein-coupled receptor UHR-1 - rat

C;Species: Rattus sp. (rat)

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000

C;Accession: I52315

R;Welch, S.K.; O'Hara, B.F.; Kilduff, T.S.; Heller, H.C.

Biochem. Biophys. Res. Commun. 209, 606-613, 1995

A;Title: Sequence and tissue distribution of a candidate G-coupled receptor cloned from rat hypothalamus.

A;Reference number: I52315; MUID:95251659; PMID:7733930

A;Accession: I52315

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-370 <RES>

A;Cross-references: GB:S77867; NID:g998527; PIDN:AAB34129.1; PID:g998528

C;Superfamily: neurokinin 1 receptor

Query Match 21.2%; Score 413.5; DB 1; Length 370;
Best Local Similarity 31.6%; Pred. No. 1.7e-27;
Matches 101; Conservative 64; Mismatches 114; Indels 41; Gaps 6;

```
Qy      44 QYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPAS 103
      |  :  ::  |  |  ||  ||||  |:  |  :  |  :  |||:  |  ||:|:|:|  |  |:|  :
Db     58 QLKGLIVMLYSIVVVVGLVGNCLLVLVIAVRRLHNVTNFLIGNLALSDVLMCAACVPLT 117
```


A;Molecule type: mRNA
 A;Residues: 1-171,'G',173,'R',175-201,'P',203-208,'A',210-381 <YAN>
 A;Cross-references: EMBL:U42389; NID:g1314329; PIDN:AAB07760.1; PID:g1314330
 C;Genetics:
 A;Gene: GDB:NPY2R
 A;Cross-references: GDB:4365607; OMIM:162642
 A;Map position: 4q31-4q31
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: appetite; G protein-coupled receptor; glycoprotein; lipoprotein;
 thiolester bond; transmembrane protein
 F;49-76/Domain: transmembrane #status predicted <TM1>
 F;87-113/Domain: transmembrane #status predicted <TM2>
 F;166-186/Domain: transmembrane #status predicted <TM4>
 F;221-237/Domain: transmembrane #status predicted <TM5>
 F;269-291/Domain: transmembrane #status predicted <TM6>
 F;305-328/Domain: transmembrane #status predicted <TM7>
 F;123-203/Disulfide bonds: #status predicted
 F;342/Binding site: palmitate (Cys) (covalent) #status predicted
 F;372/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.7%; Score 404; DB 2; Length 381;
 Best Local Similarity 27.8%; Pred. No. 1.1e-26;
 Matches 104; Conservative 71; Mismatches 133; Indels 66; Gaps 9;

Qy	3	PSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVALV	62
		:: : : : :: : : ::	
Db	24	PQTTPRGEL-----VPDPEPELI-----DSTKLIIEVQVVLILAYCSIILLGVI	66
Qy	63	GNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVI	122
		: : : : : : : : ::	
Db	67	GNSLVIHVVIKFSMRTVTNFFIANLAVADLLVNTLCLPFTLTYYTLMGWKMGVPLCHLV	126
Qy	123	PYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIILGI-WAVSLAIMVPQAA	181
		:: : : : :: : : :	
Db	127	PYAQGLAVQVSTITLTVIALDRHRCIVYHLESK-ISKRISFLIIGLAWGISALLASPLAI	185
Qy	182	VMECS--SVLPELANRTRLFVSCDERWADD---LYPKIYHSCFFIVTYLAPLGLMAMAYF	236
		:: : : : : : : : : :	
Db	186	FREYSLIEIIPDFE-----IVACTEKWPGEEKSIYGTVYSLSSLLILYVPLPLGIISFSYT	240
Qy	237	QIFRKLWGRQIPGTTTSALVRNWKRPDQGLDLEQGLSGEPQPRGRAFLAEVKQMRARRKT	296
		: : : : : : : : : : :	
Db	241	RIWSKLNHVSPGA-----ANDHYHQRQKT	266
Qy	297	AKMLMVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPI	356
		: : : : : : : : : :	
Db	267	TKMLVCVVVFVAVSWLP---LHAFQLAVDIDSQVLDLKEYKLIFTVFHIIAMCSTFANPL	323
Qy	357	IYNFLSGCKEKSIV	370
		: : : : :	
Db	324	LYGWMNSNYRKAFL	337

RESULT 4
 S50150
 gastric CCK-A receptor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)

C;Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 20-Apr-2000
 C;Accession: S50150
 R;Reuben, M.; Rising, L.; Prinz, C.; Hersey, S.; Sachs, G.
 Biochim. Biophys. Acta 1219, 321-327, 1994
 A;Title: Cloning and expression of the rabbit gastric CCK-A receptor.
 A;Reference number: S50150; MUID:95002144; PMID:7918628
 A;Accession: S50150
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-427 <REU>
 C;Superfamily: neurokinin 1 receptor

Query Match 20.1%; Score 391; DB 2; Length 427;
 Best Local Similarity 28.8%; Pred. No. 1.6e-25;
 Matches 110; Conservative 79; Mismatches 149; Indels 44; Gaps 11;

```

Qy      8 GAQMGVPPGSREPSVPVPPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGN 64
      |  |::|  |  ::| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      9 GNASGIPP-----PCELGLDNETLFCLDQP---PPSKEWQPAVQILLYSLIFLLSVLGN 59

Qy     65 TLVCLAVWRNHMRTVTNRYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPY 124
      |||  : ||  ||||| |::|::|::|  |::|::|::|  |::|::|::|  |::|::|::|  |
Db     60 TLVITVLIRNKRMRVTNIFLLSLAISDLMLCLFCMPFNLIPLNLLKDFIFGSALCKTTTY 119

Qy    125 LQAVSVSVAVLTLSFIALDRWYAICHPLLEK--STARRARGSILGIWAVSLAIMVPQAAV 182
      |  |||: | |  |::|: || | |  :  |  |  |  |  |  |  |  |  |  |  |
Db    120 LMGTSVSVSTLNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFAIMTPYPIY 179

Qy    183 MECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKL 242
      |:::|  :  ::|  |:  :::|  :  :::|  :  :::|  |  :  :||  |  : |
Db    180 ---SNLVPFTKTNNQTANMCRFLLPDVMQQAHTFLLLILFLIPGIVMMVAYGMISLEL 236

Qy    243 W-GRQIPGTTSALVRNWK-----RPSDQLGDLEQGLSGEPQPRGRA 282
      : | :  :  : |  :  : |  :  : |  :  : |  :  : |  :  : |  :  : |
Db    237 YQGIKFDASQKKSARKERKASTGSGRFEDNDGCYLQRSKPTRQL-ELQQ-LSGGGGGRVSR 294

Qy    283 F--LAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACF 340
      :  :  |:::  :|||:::|  ||::|  |  :  :  :  :  :  :  :  :  :
Db    295 IHSSSSAAALMAKKRVIRMLMVIVLFFLCWMPIFSANAWRAYDTV---SAERRLSGTPI 351

Qy    341 TFSHWLVYANSAANPIIYNFLS 362
      :|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    352 SFILLLSYTSSCVNPIIYCFMN 373

```

RESULT 5

JQ1517

neurokinin 3 receptor - human

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Homo sapiens (man)

C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004

C;Accession: JQ1517; S20435; S21237

R;Huang, R.R.C.; Cheung, A.H.; Mazina, K.E.; Strader, C.D.; Fong, T.M.

Biochem. Biophys. Res. Commun. 184, 966-972, 1992

A;Title: cDNA sequence and heterologous expression of the human neurokinin-3 receptor.

A;Reference number: JQ1517; MUID:92246993; PMID:1374246

A;Accession: JQ1517
 A;Status: nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-465 <HUA>
 A;Cross-references: UNIPROT:P29371; GB:M89473; NID:g189223; PIDN:AAA36366.1; PID:g189224
 A;Experimental source: brain
 R;Buell, G.; Schulz, M.F.; Arkinstall, S.J.; Maury, K.; Missotten, M.; Adami, N.; Talabot, F.; Kawashima, E.
 FEBS Lett. 299, 90-95, 1992
 A;Title: Molecular characterisation, expression and localisation of human neurokinin-3 receptor.
 A;Reference number: S20435; MUID:92183914; PMID:1312036
 A;Accession: S20435
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-2,'I',4-62,'R',64-465 <BUE>
 A;Cross-references: GB:S86392; NID:g246908; PIDN:AAB21706.1; PID:g246909
 R;Takahashi, K.; Tanaka, A.; Hara, M.; Nakanishi, S.
 Eur. J. Biochem. 204, 1025-1033, 1992
 A;Title: The primary structure and gene organization of human substance P and neuromedin K receptors.
 A;Reference number: S21188; MUID:92201186; PMID:1312928
 A;Accession: S21237
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-438,'F',440-465 <TAK>
 A;Cross-references: GB:X65172; NID:g35022; PIDN:CAA46291.1; PID:g825695
 C;Comment: The endogenous ligand of this receptor is neurokinin 3 (neuromedin K), one of the peptides in the mammalian tachykinin system.
 C;Genetics:
 A;Gene: GDB:TACR3
 A;Cross-references: GDB:9599126
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; transmembrane protein
 F;83-111/Domain: transmembrane #status predicted <TM1>
 F;122-147/Domain: transmembrane #status predicted <TM2>
 F;160-181/Domain: transmembrane #status predicted <TM3>
 F;202-221/Domain: transmembrane #status predicted <TM4>
 F;247-272/Domain: transmembrane #status predicted <TM5>
 F;300-321/Domain: transmembrane #status predicted <TM6>
 F;333-355/Domain: transmembrane #status predicted <TM7>
 F;23,50,73/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;158-233/Disulfide bonds: #status predicted

Query Match 19.7%; Score 383.5; DB 1; Length 465;
 Best Local Similarity 27.8%; Pred. No. 7.5e-25;
 Matches 103; Conservative 69; Mismatches 137; Indels 61; Gaps 11;

Qy	4	SATPGAQMGVPPGSREPSVPDPYEDEFRLYLWRDYLYPEQYEWVLIAAYVAVFVVALVG	63
		:: :: : :::: ::	
Db	52	SSSPSA-LGLPVASPAQSPWANLTNQFVQPSWRIAL-----WSL--AYGVVAVAVLG	102
Qy	64	NTLVCLAVWRNHMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFVGHALCKVIP	123
		: : : : : : : : :	
Db	103	NLIVIWIILAHKRMRTVTNYFLVNLAFSASMAAFNTLVNFIYALHSEWYFGANYCRFQN	162

Qy 124 YLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAVM 183
 : : | : : : | : | : | : : | : | : : | :
 Db 163 FFPITAVFASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLYS 222
 Qy 184 ECSSVLPELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 : : | : | : | : | : | : | : | : | : | :
 Db 223 K-TKVMP---GRT----LCFVQWPEG--PKQHFTYHIIIVILVYCFPLLMGITYTIVGI 272
 Qy 241 KLWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 | | | : | | | : | : | : | : | : | : | :
 Db 273 TLWGGEIPGDTCDKYH-----EQLKAKRKVVMM 301
 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY-- 358
 : : | : : | : | : | : : : : : : | : | : : | : | :
 Db 302 IIVVMTFAICWLPYHIYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSSMTYNPIIYCC 358
 Qy 359 ---NFLSGCK 365
 : : | : | :
 Db 359 LNKRFRAFGEK 368

RESULT 6

S17783

tachykinin receptor homolog DTKR - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 22-Nov-1996 #sequence_revision 22-Nov-1996 #text_change 09-Jul-2004

C;Accession: S17783

R;Li, X.J.; Wolfgang, W.; Wu, Y.N.; North, R.A.; Forte, M.

EMBO J. 10, 3221-3229, 1991

A;Title: Cloning, heterologous expression and developmental regulation of a *Drosophila* receptor for tachykinin-like peptides.

A;Reference number: S17783; MUID:92007772; PMID:1717263

A;Accession: S17783

A;Molecule type: mRNA

A;Residues: 1-519 <LIX>

A;Cross-references: UNIPROT:P30975; EMBL:X62711; NID:g8505; PIDN:CAA44595.1; PID:g8506

A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in lacking 481-Gly

C;Genetics:

A;Gene: FlyBase:Takr99D

A;Cross-references: FlyBase:FBgn0004622

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; neurotransmitter receptor; transmembrane protein

Query Match 19.6%; Score 382.5; DB 2; Length 519;

Best Local Similarity 27.4%; Pred. No. 1e-24;

Matches 106; Conservative 61; Mismatches 147; Indels 73; Gaps 10;

Qy 3 PSATPGAQMGVPPGSREPS-----PVPPDYED-----EFLRYLWRDYL 41
 | | | | | | | | | : | | |
 Db 45 PCRTLARSSPYPPVSEFNHSQTLSTDQPAVGDDVEDAAASMETGSAFVVPWWRQVL- 103
 Qy 42 PKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLP 101
 | : : : : | | : | | | | | | | | : | : : : :

Db 104 -----WSIL--FGGMVIVATGGNLIVVWIVMTTKRMRTVTNYFIVNLSIADAMVSSLNVT 156

Qy 102 ASLLVDITESWLFEGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRA 161
: : | | | : : : | : | | | : : | | : : |

Db 157 FNYYYMLDSDWPFGEFYCKLSQFIAMLSICASVFTLMAISIDRYVAIRPLQPRMSKRCN 216

Qy 162 RGSILGIWAVSLAIMVPPQAAVMECSSV-LPELANRTRLFSVCDERWAD-----DLYPKIY 215
| | | | : | : | : | | | | : |

Db 217 LAIAAVIWLASTLISCPMMIIRTEEVFVRGLSNRT----VCYPEWPDGPTNHSTMESLY 272

Qy 216 HSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGE 275
: | : | | : | : | : | : | : | : |

Db 273 NILIIILTYFLPIVSMVTYTSRVGIELWGSK-----TIGE 307

Qy 276 PQPRGRAFLAEVKQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFQASDREA 335
| | : | : | : | : | : | : | : | : | : |

Db 308 CTPR-----QVENVRSKRRVVKMMIVVVLIFAICWLPFHSYFIITSCYPAITEAPFIQE 361

Qy 336 VYACFTFSHWLVYANSAANPIIYNFLS 362
: | : | : | | | : : |

Db 362 LYLAI---YWLAMSNSMYNPIIYCWMN 385

RESULT 7

A34916

neurokinin 3 receptor - rat

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004

C;Accession: A34916

R;Shigemoto, R.; Yokota, Y.; Tsuchida, K.; Nakanishi, S.

J. Biol. Chem. 265, 623-628, 1990

A;Title: Cloning and expression of a rat neuromedin K receptor cDNA.

A;Reference number: A34916; MUID:90110113; PMID:2153106

A;Accession: A34916

A;Molecule type: mRNA

A;Residues: 1-452 <SHI>

A;Cross-references: UNIPROT:P16177; GB:J05189; NID:g205670; PIDN:AAA41688.1;

PID:g205671

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; glycoprotein; membrane protein

Query Match 19.6%; Score 382; DB 2; Length 452;

Best Local Similarity 27.8%; Pred. No. 9.7e-25;

Matches 101; Conservative 65; Mismatches 137; Indels 60; Gaps 9;

Qy 11 MGVPPGSREPSVPPDYEDFLRYLWRDYLYPEQYEWVLIAAYVAVFVVALVGNTLVCLA 70
: | : | : | : | : | : | : | : | : | : | : |

Db 45 LGLPATTQAPSQVRANLTNQFVQPSWRIAL-----WSL--AYGLVAVAVFGNLIVIWI 96

Qy 71 VWRNHHMRTVTNYFIVNLSIADVLVTAICLPASLLVDITESWLFEGHALCKVIPYLQAVSV 130
: : | | | | : | : | : : : | | : : |

Db 97 ILAHKRMRTVTNYFLVNLAFSASVAEFTLNFTYGLHSEWYFGANYCRFQNFPPITAV 156

Qy 131 SVAVLTLSFIALDRWYAICHPLLEFKSTARRAGSILGIWAVSLAIMVPPQAAVMECSSLVP 190
: : : : | : | : | : : | : | : : | : |

Db 157 FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLY----SKIK 212

```

Qy      191 ELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQI 247
      : ||      :| :| : ||      ||      | : | || :| : | : ||| :|
Db      213 VMPGRT----LCYVQWPEG--PKQHFTYHIIIVILVYCFPLLIMGVITYTIVGITLWGGEI 266

Qy      248 PGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVLLLVF 307
      || |
Db      267 PGDTCDKYH-----EQLKAKRKVVKMMIIVVVTF 295

Qy      308 ALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIY-----NFLS 362
      |:|:| | :| :: : : ||      | || :: : ||||      | :
Db      296 AICWLPYHVYFILTAIYQQLNRWKYIQQVYLA---SEFLAMSSTMYNPIIYCCLNKRFR 352

Qy      363 GCK 365
      | |
Db      353 GFK 355

```

RESULT 8

JC2459

gastrin/cholecystokinin B receptor - rabbit

C;Species: *Oryctolagus cuniculus* (domestic rabbit)

C;Date: 21-Feb-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004

C;Accession: JC2459

R;Blandizzi, C.; Song, I.; Yamada, T.

Biochem. Biophys. Res. Commun. 202, 947-953, 1994

A;Title: Molecular cloning and structural analysis of the rabbit gastrin/CCKB receptor gene.

A;Reference number: JC2459; MUID:94324990; PMID:8048969

A;Accession: JC2459

A;Molecule type: mRNA

A;Residues: 1-452 <BLA>

A;Cross-references: UNIPROT:P46627; GB:L31548; NID:g495663; PIDN:AAA31194.1; PID:g495665

C;Genetics:

A;Introns: 49/1; 133/1; 216/2; 273/1

C;Superfamily: neurokinin 1 receptor

C;Keywords: receptor; transmembrane protein

F;56-79/Domain: transmembrane #status predicted <TM1>

F;85-104/Domain: transmembrane #status predicted <TM2>

F;130-149/Domain: transmembrane #status predicted <TM3>

F;169-187/Domain: transmembrane #status predicted <TM4>

F;217-237/Domain: transmembrane #status predicted <TM5>

F;339-359/Domain: transmembrane #status predicted <TM6>

F;381-400/Domain: transmembrane #status predicted <TM7>

Query Match 19.5%; Score 379.5; DB 2; Length 452;

Best Local Similarity 27.2%; Pred. No. 1.6e-24;

Matches 100; Conservative 69; Mismatches 123; Indels 75; Gaps 9;

```

Qy      48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
      : : | :|::: || | : : : : :| || |:::|:::|:| : | :| :
Db      54 IRVTLYAVIFLMSVGGNIIIVVLGLSRRRLRTVTFNAFLSLAVSDLLAVACMPFTLLPN 113

Qy      108 ITESWLFGHALCKVIPYLAQVSVSVAVLTLSFIALDRWYAICHPLLEK--STARRARGSI 165
      : ::|| :|| : || |||| :| :| ||:|: ||| || : | | |
Db      114 LMGTFFIGTVICKAVSYLMGVSVSSTLSLVAIALERYSAICRPLQARVWQTRSHAARVI 173

```

Qy 166 LGIWAVSLAIMVPQAAVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYL 225
 | | : | : || | | : | | : : :
 Db 174 LATWLLSGLLMVPYPVYTAVQPVGPRVLQ-----CVHRWPSARVRQTWSVLLLLLLLLFF 226

Qy 226 APLGLMAMAYFQIFRKLW-----GRQIPGTTTSALVRNWKRP 261
 | : || : || | | : | : | | |
 Db 227 VPGVVMAYAYGLISRELYLGLRFDSDSSESQSRVRGQGGLPGGAAPG-----P 275

Qy 262 SDQLGDL--EQGLSGE-----PQPRGRAFL-----AEVKQMRARR 294
 | | | | : || : || | | | | | : | : | : | :
 Db 276 VHQNGRCRPEAGLAGEDGDGCYVQLPRSRPALELSALTAPISGPGPGPRPAQAK-LLAKK 334

Qy 295 KTAKMLMVLLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAAN 354
 : : || : || : || : || : | : | : | | | : |
 Db 335 RVVRMLLVIVVLFFMCWLPVYSANTWRAFDG---PGAHRALSGAPISFIHLLSYASACVN 391

Qy 355 PIIYNFL 361
 | : | | :
 Db 392 PLVYCFM 398

RESULT 9

JC7809

sulfakinin receptor protein, DSK-R1 - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 03-Jun-2002 #sequence_revision 03-Jun-2002 #text_change 09-Jul-2004

C;Accession: JC7809

R;Kubiak, T.M.; Larsen, M.J.; Burton, K.J.; Bannow, C.A.; Martin, R.A.; Zantello, M.R.; Lowery, D.E.

Biochem. Biophys. Res. Commun. 291, 313-320, 2002

A;Title: Cloning and functional expression of the first *Drosophila melanogaster* sulfakinin receptor DSK-R1.

A;Reference number: JC7809; PMID:11846406; MUID:21835488

A;Accession: JC7809

A;Molecule type: mRNA

A;Residues: 1-584 <KUB>

A;Cross-references: UNIPROT:Q7M3J6; GB:AX128640

C;Comment: This receptor, the first functionally active orphan *Drosophila* sulfakinin G-protein-coupled receptor, with seven transmembrane domains, has the possible roles in insect brain and/or gut functions.

C;Genetics:

A;Gene: dsk-r1

A;Map position: 17

F;115-139/Domain: transmembrane region #status predicted <TMR1>

F;149-167/Domain: transmembrane region #status predicted <TMR2>

F;189-207/Domain: transmembrane region #status predicted <TMR3>

F;229-250/Domain: transmembrane region #status predicted <TMR4>

F;275-300/Domain: transmembrane region #status predicted <TMR5>

F;431-454/Domain: transmembrane region #status predicted <TMR6>

F;467-491/Domain: transmembrane region #status predicted <TMR7>

Query Match 19.5%; Score 379; DB 2; Length 584;

Best Local Similarity 25.9%; Pred. No. 2.3e-24;

Matches 115; Conservative 72; Mismatches 141; Indels 116; Gaps 14;

Qy 3 PSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVALV 62

F;334-357/Domain: transmembrane #status predicted <TM6>
F;380-398/Domain: transmembrane #status predicted <TM7>
F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.3%; Score 376.5; DB 2; Length 450;
Best Local Similarity 29.1%; Pred. No. 2.8e-24;
Matches 102; Conservative 67; Mismatches 135; Indels 47; Gaps 9;

Qy 48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
: | | :|::: || | : : : : : |||| |::|::|:|: | :| :|| :
Db 56 IRITLYAVIFLMSIGGNMLIIVVLGLSRRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLPN 115

Qy 108 ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEK--STARRARGSI 165
: ::|| :|| : || ||||: | | |||:| :|| | | : | | |
Db 116 LMGTFFIFGTVICKAVSYLMGVSVSVSTLNLVAIALERYSAICRPLQARVWQTRSHAARVI 175

Qy 166 LGIWAVSLAIMVPQAAVMECSSVLPELANRTRLFSSVCDERWADDLPKIYHSCFFIVTYL 225
| | :| :|| | | : | | | : : : : :
Db 176 LATWLLSGLLMVPYPVYTVVQPVGPRVLQ-----CMHRWPSARVRQTWSVLLMLLFF 228

Qy 226 APLGLMAMAYFQIFRKLW-GRQIPG-----TTSALVRNW-----KRPSDQLGDLEQ-G 271
| :||:| | | |:|: | : | | : || | | | |
Db 229 IPGVVMAVAYGLISRELYLGLRFDGDNDSDTQSRVRNQGGPLPGGTAPGPVHQNGGCRHVT 288

Qy 272 LSGEPQ-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLVFALC 310
: || | | | : | : : |::: :||:|::| | |
Db 289 VAGEDNDGCYVQLPRSRLEMTTLTPTPGPLASANQAKLLAKKRVVRMLLVIVLLFFLC 348

Qy 311 YLPISVLNVLKRVFQMFQASDREAVYACFTFSHWLVYANSAANPIIYNFL 361
: || | | : | | | | | : | | : | : | :
Db 349 WLPIYSANTWCAFDG---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM 396

RESULT 11

S55524

neurokinin 3 receptor - mouse (fragment)

N;Alternate names: neuromedin K receptor; NK-3 receptor

C;Species: Mus musculus (house mouse)

C;Date: 01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004

C;Accession: S55524; I73045

R;Maroteaux, L.

submitted to the EMBL Data Library, June 1995

A;Reference number: S55524

A;Accession: S55524

A;Molecule type: mRNA

A;Residues: 1-385 <MAR>

A;Cross-references: UNIPROT:P47937; EMBL:X87823; NID:g861055; PIDN:CAA61088.1;
PID:g861056

R;Cook, G.A.; Elliott, D.; Metwali, A.; Blum, A.M.; Sandor, M.; Lynch, R.;
Weinstock, J.V.

J. Immunol. 152, 1830-1835, 1994

A;Title: Molecular evidence that granuloma T lymphocytes in murine
schistosomiasis mansoni express an authentic substance P (NK-1) receptor.

A;Reference number: I56216; MUID:94165478; PMID:8120392

A;Accession: I73045

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 103-197,'S',199-266,'P',268-328 <COO>
A;Cross-references: GB:L27827; NID:g450288; PIDN:AAA17893.1; PID:g480780
C;Superfamily: neurokinin 1 receptor

Query Match 19.3%; Score 376; DB 2; Length 385;
Best Local Similarity 27.8%; Pred. No. 2.6e-24;
Matches 101; Conservative 64; Mismatches 138; Indels 60; Gaps 9;

```
Qy      11  MGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLA 70
          :|:| |:||| : :|:: || | | | | | | | | | | | | | |
Db      45  LGLPVTSQLAPSQVRDNLTNQFVQPSWRIAL-----WSL--AYGLVVAVAVFGNLIWIWI 96

Qy      71  VWRNHMRTVTNRYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCKVIPYLQAVSV 130
          : : ||||| |:|:| | | : : : | || |: : : |
Db      97  ILAHKRMRTVTNRYFLVNLAFSDASVAAFNTLVNFIYGVHSEWYFGANYCRFQNFPPITAV 156

Qy     131  SVAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIILGIWAVSLAIMVPQAAVMECSSVLP 190
          :: :: |:|:| | | | : :| : | | | : : | | :
Db     157  FASIYSMTAIAVDRYMAIIDPLKPRLSATATKIVIGSIWILAFLLAFPQCLY----SKIK 212

Qy     191  ELANRTRLFSVCDERWADDLYPK---IYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQI 247
          : || :| :| : || || |: | || :| : | : ||| :|
Db     213  VMFGRT---LCYVQWPEG--PKQHFTYHIIVIIILVYCFPLLIMGVTTYTIVGITLWGGEI 266

Qy     248  PGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKMLMVVLLVF 307
          | | :|:|:| | | | | | | | | | | | | | |
Db     267  LGDTCCKYH-----EQLKAKRKVKVMMIIVVTF 295

Qy     308  ALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIY-----NFLS 362
          |:|:| | :| : : : : || | | | : : | | | | :
Db     296  AICWLPYHVYFILTAIYQQLNRWKYIQQVYLA---SFWLAMSSTMYNPIIYCCLNKRFR 352

Qy     363  GCK 365
          | |
Db     353  GFK 355
```

RESULT 12

JN0692

cholecystokinin type A receptor - human

C;Species: Homo sapiens (man)

C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C;Accession: JN0692; JN0590

R;de Weerth, A.; Pisegna, J.R.; Huppi, K.; Wank, S.A.

Biochem. Biophys. Res. Commun. 194, 811-818, 1993

A;Title: Molecular cloning, functional expression and chromosomal localization of the human cholecystokinin type A receptor.

A;Reference number: JN0692; MUID:93343941; PMID:8343165

A;Accession: JN0692

A;Molecule type: mRNA

A;Residues: 1-428 <DEW>

A;Cross-references: UNIPROT:P32238; GB:L19315; NID:g306595; PIDN:AAA02819.1; PID:g306596

A;Experimental source: gallbladder

R;Ulrich, C.D.; Ferber, I.; Holicky, E.; Hadac, E.; Buell, G.; Miller, L.J.
Biochem. Biophys. Res. Commun. 193, 204-211, 1993

A;Title: Molecular cloning and functional expression of the human gallbladder cholecystokinin A receptor.
A;Reference number: JN0590; MUID:93277552; PMID:8503909
A;Accession: JN0590
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-428 <ULR>
A;Cross-references: GB:L13605; NID:g306490; PIDN:AAA35659.1; PID:g306491
A;Experimental source: gallbladder
C;Comment: This protein has diverse physiological roles in the gastrointestinal system where it mediates pancreatic growth and enzyme secretion, smooth muscle contraction of the gallbladder and stomach, and secretion from gastric mucosal cells.
C;Genetics:
A;Gene: GDB:CCKAR
A;Cross-references: GDB:141927; OMIM:118444
A;Map position: 4pter-4qter
C;Superfamily: neurokinin 1 receptor
C;Keywords: G protein-coupled receptor; glycoprotein; hormone receptor; phosphoprotein; transmembrane protein
F;40-67/Domain: transmembrane #status predicted <TM1>
F;78-104/Domain: transmembrane #status predicted <TM2>
F;116-137/Domain: transmembrane #status predicted <TM3>
F;158-178/Domain: transmembrane #status predicted <TM4>
F;208-234/Domain: transmembrane #status predicted <TM5>
F;314-332/Domain: transmembrane #status predicted <TM6>
F;350-369/Domain: transmembrane #status predicted <TM7>
F;10,24,190,299/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;245,249,260,290/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F;256/Binding site: phosphate (Ser) (covalent) (by protein kinase A) #status predicted

Query Match 19.2%; Score 373.5; DB 2; Length 428;
Best Local Similarity 28.3%; Pred. No. 4.8e-24;
Matches 106; Conservative 77; Mismatches 154; Indels 37; Gaps 10;

```

Qy      16 GSREPSVPPDYEDFLRYLWRDYLYPKQYEW---VLIAAYVAVFVVALVGNTLVCLAVW 72
      ||      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      11 GSNITPPCELGLENETLFLCL--DQPRPSK-EWQPAVQILLYSLIFLLSVLGNTLVITVLI 67

Qy      73 RNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSV 132
      ||  |||||  |::|::|::|  |::|::|::|  |::|::|::|  |::|::|::|
Db      68 RNKRMRTVTNIFLLSLAVSDLMLCLFCMPFNLIPLNLLKDFIFGSAVCKTTTYFMGTSVSV 127

Qy     133 AVLTLSEFIALDRWYAICHPLLFK--STARRAGSILGIWAVSLAIMVPQAAMVMECSSLVP 190
      :  |  |::|: ||| ||  :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     128 STFNLVAISLERYGAICKPLQSRVWQTKSHALKVIAATWCLSFITIMTPYPIY---SNLVP 184

Qy     191 ELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLW----- 243
      |  :  ::|  :|:  :|:  ::|:  ::|:  ::|:  ::|:  ::|:  ::|:
Db     185 FTKNNNQ TANMCRFLPNQDVMQSWHTFLLLILFLIPGIVMMVAYGLISLELYQGIKFEA 244

Qy     244 -----GRQIPGTTSA-----LVRNWKRPSDQLGDLEQGLSGEPQPRGR-AFLAEVK 288
      :  |  |||:  :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     245 SQKKSAKERKPSTTSSGKYEDSDGCYLQKTRPPRKL-ELRQLSTGSSSRANRIRSNSSAA 303

```

QY 289 QMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVY 348
 : |::: :||:|:::| ||::|| | : :::| :| | |
 Db 304 NLMAKKRVIRMLIVIVVLFFLCWMPIFSANAWR---AYDTASAERRLSGTPISFILLLSY 360
 QY 349 ANSAANPIIYNFLS 362
 :| |||| |::
 Db 361 TSSCVNPIIYCFMN 374

RESULT 13

A46195

cholecystokinin B receptor subtype - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A46195

R;Wank, S.A.; Pisegna, J.R.; de Weerth, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 8691-8695, 1992

A;Title: Brain and gastrointestinal cholecystokinin receptor family: structure and functional expression.

A;Reference number: A46195; MUID:92409582; PMID:1528881

A;Accession: A46195

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-452 <WAN>

A;Cross-references: UNIPROT:P30553; GB:M99418; NID:g203459; PIDN:AAA40925.1; PID:g203460

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIN:114083, NCBIP:114084)

C;Superfamily: neurokinin 1 receptor

C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.2%; Score 373.5; DB 2; Length 452;
 Best Local Similarity 27.2%; Pred. No. 5.1e-24;
 Matches 96; Conservative 73; Mismatches 135; Indels 49; Gaps 8;

QY 48 VLIAAYVAVFVVALVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
 : | | :|::: || | : : : : |||| |::|:::|::| :| :|| :
 Db 56 IRITLYAVIFLMSVGGNVLIIVVLGLSRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLPN 115
 QY 108 ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEK--STARRARGSI 165
 : :::|| :|| | || ||||: | | ||:|: || | | : | | |
 Db 116 LMGTFIFGTVICKAISYLMGVSVSVSTLNLVAIALERYSAICRPLQARVWQTRSHAARVI 175
 QY 166 LGIWAVSLAIMVPQAAVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYL 225
 | . | :| :|| | | : | | : : : : : :
 Db 176 LATWLLSGLLMVPYPVYTMVQPVGPRVLQ-----CMHRWPSARVQQTWSVLGLLLFF 228
 QY 226 APLGLMAMAYFQIFRKLW-GRQIPGTTSALVRNWKRPDQL-----GDLEQ----- 270
 | :|:| | | | : | | : : | | | : |
 Db 229 IPGVVIAVAYGLISRELYLGLHFDGENDSETQSRARNQGGLPGGAAPGPVHQNGGCRPVT 288
 QY 271 GLSGEPQ-----PRGRAFLAEV-----KQMRARRKTAKMLMVLLVFA 308
 :|| | | : : : : |::: |::|:::|
 Db 289 SVAGEDSDGCCVQLPRSRLEMTTLTPTPGVPVGPVPRNQAKLLAKKRVVRMLLIVIVLLFF 348
 QY 309 LCYLPISVLNVLKRVMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFL 361
 ||::|: :| : | : | :| | | : : ||::| :

RESULT 14

A47430

gastrin/cholecystokinin receptor B, short splice form - human

N;Alternate names: CCK-B/gastrin receptor; cholecystokinin-B/gastrin receptor
C;Species: Homo sapiens (man)

C;Date: 25-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A47430; JC1352; A46645; A48262

R;Ito, M.; Matsui, T.; Taniguchi, T.; Tsukamoto, T.; Murayama, T.; Arima, N.;
Nakata, H.; Chiba, T.; Chihara, K.

J. Biol. Chem. 268, 18300-18305, 1993

A;Title: Functional characterization of a human brain cholecystokinin-B
receptor. A trophic effect of cholecystokinin and gastrin.

A;Reference number: A47430; MUID:93352657; PMID:8349705

A;Accession: A47430

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-447 <ITO>

A;Cross-references: UNIPROT:P32239; GB:D13305; NID:g436039; PIDN:BAA02564.1;
PID:g436040

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:136448)

R;Pisegna, J.R.; de Weerth, A.; Huppi, K.; Wank, S.A.

Biochem. Biophys. Res. Commun. 189, 296-303, 1992

A;Title: Molecular cloning of the human brain and gastric cholecystokinin
receptor: Structure, functional expression and chromosomal localization.

A;Reference number: JC1352; MUID:93080572; PMID:1280419

A;Accession: JC1352

A;Molecule type: mRNA

A;Residues: 1-447 <PIS>

A;Cross-references: GB:L04473; NID:g179997; PIDN:AAA35660.1; PID:g179998

A;Experimental source: brain, gastric

R;Lee, Y.M.; Beinborn, M.; McBride, E.W.; Lu, M.; Kolakowski Jr., L.F.; Kopin,
A.S.

J. Biol. Chem. 268, 8164-8169, 1993

A;Title: The human brain cholecystokinin-B/gastrin receptor. Cloning and
characterization.

A;Reference number: A46645; MUID:93216795; PMID:7681836

A;Accession: A46645

A;Status: nucleic acid sequence not shown; not compared with conceptual
translation

A;Molecule type: mRNA

A;Residues: 1-447 <LEE>

A;Cross-references: GB:L08112; NID:g306488; PIDN:AAA35657.1; PID:g306489

A;Experimental source: brain

A;Note: sequence extracted from NCBI backbone (NCBIP:129156)

R;Song, I.; Brown, D.R.; Wiltshire, R.N.; Gantz, I.; Trent, J.M.; Yamada, T.
Proc. Natl. Acad. Sci. U.S.A. 90, 9085-9089, 1993

A;Title: The human gastrin/cholecystokinin type B receptor gene: alternative
splice donor site in exon 4 generates two variant mRNAs.

A;Reference number: A48262; MUID:94022320; PMID:8415658

A;Accession: A48262

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-447 <RES>

A;Cross-references: GB:L10822; NID:g406075; PIDN:AAC37528.1; PID:g406076
 C;Genetics:
 A;Gene: GDB:CCKBR
 A;Cross-references: GDB:136457; OMIM:118445
 A;Map position: 11p15.5-11p15.4
 A;Introns: 51/1; 135/1; 218/2; 271/1
 C;Superfamily: neurokinin 1 receptor
 C;Keywords: alternative splicing; G protein-coupled receptor; glycoprotein;
 hormone receptor; phosphoprotein; transmembrane protein
 F;57-81/Domain: transmembrane #status predicted <TM1>
 F;91-116/Domain: transmembrane #status predicted <TM2>
 F;131-150/Domain: transmembrane #status predicted <TM3>
 F;171-192/Domain: transmembrane #status predicted <TM4>
 F;219-243/Domain: transmembrane #status predicted <TM5>
 F;334-354/Domain: transmembrane #status predicted <TM6>
 F;369-392/Domain: transmembrane #status predicted <TM7>
 F;7,30,36/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F;82,154,300,442/Binding site: phosphate (Ser) (covalent) #status predicted
 F;127-205/Disulfide bonds: #status predicted
 F;321/Binding site: phosphate (Thr) (covalent) #status predicted

Query Match 19.2%; Score 373; DB 2; Length 447;
 Best Local Similarity 27.6%; Pred. No. 5.6e-24;
 Matches 98; Conservative 70; Mismatches 129; Indels 58; Gaps 8;

```

Qy      48 VLIAAYVAVFVVALVGNLTLCVAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVD 107
      : | | :|::: || | : : : :| || | :|::|::|::|: |::|::|
Db      56 IRITLYAVIFLMSVGGNMLIIVVLGLSRRLRTVTNAFLLSLAVSDLLLAVACMPFTLLPN 115

Qy      108 ITESWLFGHALCKVIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFK--STARRARGSI 165
      : ::|| :|| : || ||||| :| | |||:| || || : | | |
Db      116 LMGTFIFGTVICKAVSYLMGVSVSVSTLSLVAIALERYSAICRPLQARVWQTRSHAARVI 175

Qy      166 LGIWAVSLAIMVPQAAMVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYL 225
      : | :| :|| | | : | || : : : :
Db      176 VATWLLSGLLMVPYPVYTQVQVGPVRLQ-----CVHRWPSARVRQTWSVLLLLLLLLFF 228

Qy      226 APLGLMAMAYFQIFRKLW-----GRQIPGTTLSALVRNWK-RPSDQLGDL 268
      | :|::| | :|: | | | :| :| :|
Db      229 IPGVMAVAYGLISRELYLGLRFDGSDSDSQSRVRNQGLPGAVHQNGRCRP----- 281

Qy      269 EQGLSGEPQ-----PRGRAFL-----AEVKQMRARRKTAKMLMVLLV 306
      | | || | | | | :|::|::|::|::|
Db      282 ETGAVGEDSDGCVQLPRSRPALELTALTAPGPGSGSRPTQAKLLAKKRVVRMLLVIVVL 341

Qy      307 FALCYLPISVLNVLKRVFQMFQASDREAVYACFTFSHWLVYANSAANPIIYNFL 361
      | ||::|: | : | : | | | ||:: ||::| |
Db      342 FFLCWLPVYSANTWRAFDG---PGAHRALSGAPISFIHLLSYASACVNPLVYCFM 393

```

RESULT 15

B40470

glucocorticoid-induced receptor precursor, short form RP23 - mouse

C;Species: Mus musculus (house mouse)

C;Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 09-Jul-2004

C;Accession: B40470

R;Harrigan, M.T.; Campbell, N.F.; Bourgeois, S.

Mol. Endocrinol. 5, 1331-1338, 1991

A;Title: Identification of a gene induced by glucocorticoids in murine T-cells: a potential G protein-coupled receptor.

A;Reference number: A40470; MUID:92123228; PMID:1663214

A;Accession: B40470

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-423 <HAR>

A;Cross-references: UNIPROT:P30731; GB:M80481; GB:M80610; NID:g193516;

PIDN:AAA17882.1; PID:g460318

C;Superfamily: neurokinin 1 receptor

Query Match 19.1%; Score 371.5; DB 2; Length 423;
Best Local Similarity 27.5%; Pred. No. 7e-24;
Matches 103; Conservative 75; Mismatches 138; Indels 59; Gaps 10;

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Qy      5 ATPGAQMGVPPGSREPSVPDPYEDEF-LRYL---WRDYLYPKQY-----EWVLIA 51
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Db      17 ATEQPQVTEHPSMEAALTGPNASSHFWANYTFSDWQNFVGRRRYGAESQNPTVKALLIV 76

Qy      52 AYVAVFVVALVGNTLVCLAVWRNHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES 111
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Db      77 AYSFTIVFSLFGNVLVCHVIFKNQRMHSATSLFIVNLAVADIMITLLNTPFTLVRFVNST 136

Qy     112 WLFGHALCKVIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIWAV 171
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Db     137 WVFQKGMCHVSRFAQYCSLHVSALTTLTAIAVDRHQVIMHPLKPRISITKGVIIYIAVIWVM 196

Qy     172 SLAIMVPQAAMVMECSSVLPELANRTRLFSVC--DERWADDLYPKIYHSCFFIVTYLAPLG 229
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Db     197 ATFFSLPHAI---CQKLFTFKYSEDIVRSLCLPDFPEPADLFWKYLDLATFILLYLLPLF 253

Qy     230 LMAMAYFQIFRKLWGRQIPGTTSALVRNWKRPDQLGDL--EQGLSGEPQPRGRAFLAEV 287
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Db     254 IISVAYARVAKKIW-----LCNTIGDVTTEQYLA----- 282

Qy     288 KQMRARRKTAKMLMVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLV 347
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Db     283 -LRRKKKTTVKMLVLVVVLFALCWFLNVCYVLLL----SSKAIHTNNALYFAF---HWFA 334

Qy     348 YANSAANPIIYNFLS 362
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Search completed: October 14, 2004, 10:56:57

Job time : 20.7804 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2004, 10:55:56 ; Search time 69.2316 Seconds
(without alignments)
1737.280 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMGVPPGSREP.....ANPTIYNFLSGCKEKSILVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1360919 seqs, 323318874 residues

Total number of hits satisfying chosen parameters: 1360919

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result %
Query

No.	Score	Match	Length	DB	ID	Description
1	1944	99.8	372	10	US-09-393-696-6	Sequence 6, Appli
2	1944	99.8	372	13	US-10-077-874-6	Sequence 6, Appli
3	1943	99.8	389	9	US-09-828-538-20	Sequence 20, Appl
4	1943	99.8	389	10	US-09-211-823C-23	Sequence 23, Appl
5	1903	97.7	369	13	US-10-077-874-4	Sequence 4, Appli
6	1903	97.7	425	9	US-09-828-538-19	Sequence 19, Appl
7	1903	97.7	425	9	US-09-828-538-24	Sequence 24, Appl
8	1903	97.7	425	10	US-09-211-823C-22	Sequence 22, Appl
9	1903	97.7	425	14	US-10-225-567A-368	Sequence 368, App
10	1903	97.7	425	14	US-10-352-684A-22	Sequence 22, Appl
11	1898	97.5	425	10	US-09-826-509-549	Sequence 549, App
12	1897	97.4	402	13	US-10-077-874-2	Sequence 2, Appli
13	1897	97.4	425	9	US-09-961-848-2	Sequence 2, Appli
14	1886	96.9	402	10	US-09-393-696-2	Sequence 2, Appli
15	1875	96.3	369	10	US-09-393-696-4	Sequence 4, Appli
16	1783	91.6	427	9	US-09-730-931-2	Sequence 2, Appli
17	1342.5	69.0	460	14	US-10-081-810-46	Sequence 46, Appl
18	1341.5	68.9	444	10	US-09-992-331-19	Sequence 19, Appl
19	1341.5	68.9	444	14	US-10-081-810-45	Sequence 45, Appl
20	1341.5	68.9	444	14	US-10-225-567A-370	Sequence 370, App
21	1341.5	68.9	444	14	US-10-262-313-19	Sequence 19, Appl
22	1341.5	68.9	444	14	US-10-060-369-11	Sequence 11, Appl
23	1341.5	68.9	444	14	US-10-178-194-2	Sequence 2, Appli
24	1341.5	68.9	444	16	US-10-768-878-19	Sequence 19, Appl
25	1340.5	68.8	444	14	US-10-282-717-2	Sequence 2, Appli
26	1336.5	68.6	444	10	US-09-826-509-551	Sequence 551, App
27	1307	67.1	263	14	US-10-278-087A-54	Sequence 54, Appl
28	485.5	24.9	430	9	US-09-866-248A-8	Sequence 8, Appli
29	485.5	24.9	430	14	US-10-225-567A-658	Sequence 658, App
30	485.5	24.9	430	16	US-10-719-587-54	Sequence 54, Appl
31	485.5	24.9	441	14	US-10-292-798-890	Sequence 890, App
32	481.5	24.7	428	9	US-09-292-973-4	Sequence 4, Appli
33	480.5	24.7	432	9	US-09-866-248A-2	Sequence 2, Appli
34	480.5	24.7	432	16	US-10-719-587-37	Sequence 37, Appl
35	476.5	24.5	420	9	US-09-866-248A-6	Sequence 6, Appli
36	476.5	24.5	420	14	US-10-060-369-9	Sequence 9, Appli
37	476.5	24.5	522	14	US-10-081-810-53	Sequence 53, Appl
38	476.5	24.5	522	14	US-10-225-567A-512	Sequence 512, App
39	476.5	24.5	522	14	US-10-255-551-2	Sequence 2, Appli
40	476.5	24.5	522	15	US-10-072-012-360	Sequence 360, App
41	476.5	24.5	522	15	US-10-072-012-361	Sequence 361, App
42	476.5	24.5	522	15	US-10-276-774-2093	Sequence 2093, Ap
43	476.5	24.5	522	17	US-10-757-262-8	Sequence 8, Appli
44	472	24.2	417	15	US-10-072-012-358	Sequence 358, App
45	453	23.3	426	9	US-09-292-973-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1

US-09-393-696-6

; Sequence 6, Application US/09393696

; Publication No. US20030022277A1

; GENERAL INFORMATION:

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; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616
; EARLIER FILING DATE: 1995-05-05
; EARLIER APPLICATION NUMBER: US08/462,509
; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 372
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-6
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Query Match          99.8%; Score 1944; DB 10; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.3e-177;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      1 MEPSATPGAQMGVPPGSRDPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
          ||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
          ||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db    301 MVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSGCKEKSIVLS 372
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Db    361 LSGCKEKSIVLS 372
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RESULT 2

US-10-077-874-6

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; Sequence 6, Application US/10077874
; Publication No. US20020115155A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
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; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/077,874
;   FILING DATE: 20-Feb-2002
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/462,509
;   FILING DATE: 05-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1D1
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 372 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-077-874-6

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Query Match          99.8%; Score 1944; DB 13; Length 372;
Best Local Similarity 99.7%; Pred. No. 5.3e-177;
Matches 371; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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        ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db     121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLEFKSTARRARGSIWAVSLAIMVPQA 180

Qy     181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db     181 AVMECSSLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

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Db      241 KIWGRQIPGTTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
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Db      301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Qy      361 LSGCKEKSIVLS 372
Db      361 LSGCKEKSIVLS 372

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RESULT 3

US-09-828-538-20

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; Sequence 20, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 389
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-20

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Query Match          99.8%; Score 1943; DB 9; Length 389;
Best Local Similarity 99.7%; Pred. No. 7e-177;
Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 361 LSGCKEKSILVLS 372
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 Db 361 LSGCKEKSILALS 372

RESULT 4

US-09-211-823C-23

; Sequence 23, Application US/09211823C

; Publication No. US20030087801A1

; GENERAL INFORMATION:

; APPLICANT: HAGEN, JAMES JOSEPH

; APPLICANT: TERRETT, JONATHAN ALEXANDER

; APPLICANT: UPTON, NEIL

; APPLICANT: PIPER, DAVID

; APPLICANT: SMITH, MARTIN IAN

; APPLICANT: KENNETT, GUY ANTHONY

; APPLICANT: PATEL, SARASWATI R.

; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS

; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR

; TITLE OF INVENTION: ANTAGONISTS THEREOF

; FILE REFERENCE: P50745

; CURRENT APPLICATION NUMBER: US/09/211,823C

; CURRENT FILING DATE: 1998-12-15

; PRIOR APPLICATION NUMBER: US 60/069,459

; PRIOR FILING DATE: 1997-12-15

; PRIOR APPLICATION NUMBER: US 60/069,785

; PRIOR FILING DATE: 1997-12-16

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 23

; LENGTH: 389

; TYPE: PRT

; ORGANISM: HOMO SAPIENS

US-09-211-823C-23

Query Match 99.8%; Score 1943; DB 10; Length 389;

Best Local Similarity 99.7%; Pred. No. 7e-177;

Matches 371; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
 |||
 Db 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
 |||

Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCK 120
 Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
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 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
 Qy 181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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 Db 181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 Qy 241 KLGWRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
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 Db 241 KLGWRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 Qy 301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 Qy 361 LSGCKEKS LVLS 372
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 Db 361 LSGCKEKS LALS 372

RESULT 5

US-10-077-874-4

; Sequence 4, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

; REGISTRATION NUMBER: 43,975

; REFERENCE/DOCKET NUMBER: PF168P1D1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 301-309-8504

; TELEFAX: 301-309-8439

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; INFORMATION FOR SEQ ID NO: 4:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 369 amino acids
;         TYPE: amino acid
;         TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-077-874-4
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Query Match          97.7%; Score 1903; DB 13; Length 369;
Best Local Similarity 100.0%; Pred. No. 4.3e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
          |||
Db    361 LSG 363
```

RESULT 6

US-09-828-538-19

```
; Sequence 19, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
; APPLICANT: Ellis, Catherine E.
; APPLICANT: Kwok, Cheni
; APPLICANT: Bodsworth, Nicola J.
; APPLICANT: Halsey, Wendy
; APPLICANT: Van Horn, Stephanie
; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
```


; PRIOR APPLICATION NUMBER: 60/088,624
 ; PRIOR FILING DATE: 1998-06-08
 ; PRIOR APPLICATION NUMBER: 60/093,726
 ; PRIOR FILING DATE: 1998-07-22
 ; PRIOR APPLICATION NUMBER: 09/328,014
 ; PRIOR FILING DATE: 1999-06-08
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 19
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-828-538-19

Query Match 97.7%; Score 1903; DB 9; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.1e-173;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLI AAYVAVFVVA 60
 |||
 Db 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLKQYEWVLI AAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
 |||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
 |||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy 181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSLPELANRTRLFSVC DERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTT SALVRNWKRP SDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 7

US-09-828-538-24
 ; Sequence 24, Application US/09828538
 ; Patent No. US20010025031A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ellis, Catherine E.
 ; APPLICANT: Kwok, Cheni
 ; APPLICANT: Bodsworth, Nicola J.
 ; APPLICANT: Halsey, Wendy
 ; APPLICANT: Van Horn, Stephanie

```

; TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
; TITLE OF INVENTION: of Use Thereof in Diagnostic Applications
; FILE REFERENCE: GH-50038-C1
; CURRENT APPLICATION NUMBER: US/09/828,538
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/088,624
; PRIOR FILING DATE: 1998-06-08
; PRIOR APPLICATION NUMBER: 60/093,726
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: 09/328,014
; PRIOR FILING DATE: 1999-06-08
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-828-538-24

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```

Query Match          97.7%; Score 1903; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        |||
Db      1 MEPSATPGAQMGVPPGSRPSPVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        |||
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
        |||
Db      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180

Qy      181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        |||
Db      181 AVMECSSVLPELANRTRLFVSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        |||
Db      241 KLWGRQIPGTTLSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        |||
Db      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
        |||
Db      361 LSG 363

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RESULT 8
US-09-211-823C-22
; Sequence 22, Application US/09211823C
; Publication No. US20030087801A1
; GENERAL INFORMATION:

```

```

; APPLICANT: HAGEN, JAMES JOSEPH
; APPLICANT: TERRETT, JONATHAN ALEXANDER
; APPLICANT: UPTON, NEIL
; APPLICANT: PIPER, DAVID
; APPLICANT: SMITH, MARTIN IAN
; APPLICANT: KENNETT, GUY ANTHONY
; APPLICANT: PATEL, SARASWATI R.
; TITLE OF INVENTION: METHODS OF TREATMENT USING NOVEL LIGANDS
; TITLE OF INVENTION: OF THE NEUROPEPTIDE RECEPTOR HFGAN72 AND AGONISTS OR
; TITLE OF INVENTION: ANTAGONISTS THEREOF
; FILE REFERENCE: P50745
; CURRENT APPLICATION NUMBER: US/09/211,823C
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: US 60/069,459
; PRIOR FILING DATE: 1997-12-15
; PRIOR APPLICATION NUMBER: US 60/069,785
; PRIOR FILING DATE: 1997-12-16
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 425
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-211-823C-22

```

```

Query Match          97.7%; Score 1903; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 5.1e-173;
Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSRPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSAVLTLFSFIALDRWYAICHPLLFKSTARRARGSIWAVSLAIMVPQA 180

Qy    181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSVLPELANRTRLSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363

```

RESULT 9
 US-10-225-567A-368
 ; Sequence 368, Application US/10225567A
 ; Publication No. US20030113798A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LifeSpan Biosciences
 ; APPLICANT: Brown, Joseph P.
 ; APPLICANT: Burmer, Glenna C.
 ; APPLICANT: Roush, Christine L.
 ; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED
 RECEPTORS (GPCRS)
 ; FILE REFERENCE: 1920-4-4
 ; CURRENT APPLICATION NUMBER: US/10/225,567A
 ; CURRENT FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 60/257,144
 ; PRIOR FILING DATE: 2000-12-19
 ; NUMBER OF SEQ ID NOS: 2292
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 368
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-225-567A-368

Query Match 97.7%; Score 1903; DB 14; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.1e-173;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MEPSATPGAQMGPVPPGSR	EPSPVPPDYED	FLRYLWRDYL	PKQYEWV	LIAAYVAVFVVA	60
Db	1	MEPSATPGAQMGPVPPGSR	EPSPVPPDYED	FLRYLWRDYL	PKQYEWV	LIAAYVAVFVVA	60
QY	61	LVGNTLVCLAVWRNHHMRT	VTNYFIVNLSLADVL	VTAICLPASLLVD	ITESWLF	GHALCK	120
Db	61	LVGNTLVCLAVWRNHHMRT	VTNYFIVNLSLADVL	VTAICLPASLLVD	ITESWLF	GHALCK	120
QY	121	VIPYLQAVSVSVAVL	TLSFIALDRWYAICH	PLLFKSTARR	AGSILGIWAV	SLAIMVPQA	180
Db	121	VIPYLQAVSVSVAVL	TLSFIALDRWYAICH	PLLFKSTARR	AGSILGIWAV	SLAIMVPQA	180
QY	181	AVMECSSVLPELANR	TRLFVCDERWADD	LYPKIYHSCFF	IVTYLAPLGLMAMAY	FQIFR	240
Db	181	AVMECSSVLPELANR	TRLFVCDERWADD	LYPKIYHSCFF	IVTYLAPLGLMAMAY	FQIFR	240
QY	241	KLWGRQIPGTTSAL	VRNWKRP	SDQLGDLEQGLSGEP	QPRGRAFLAEVKQMR	ARRKTAKML	300
Db	241	KLWGRQIPGTTSAL	VRNWKRP	SDQLGDLEQGLSGEP	QPRGRAFLAEVKQMR	ARRKTAKML	300
QY	301	MVLLLVFALCYLPIS	VNLVLRVFGMFRQASD	REAVYACFTFS	HWLVYANSAANPII	YNF	360
Db	301	MVLLLVFALCYLPIS	VNLVLRVFGMFRQASD	REAVYACFTFS	HWLVYANSAANPII	YNF	360
QY	361	LSG	363				
Db	361	LSG	363				

RESULT 10
 US-10-352-684A-22
 ; Sequence 22, Application US/10352684A
 ; Publication No. US20030215452A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Millennium Pharmaceuticals Inc.
 ; APPLICANT: Carroll, Joseph M.
 ; APPLICANT: Healy, Aileen
 ; APPLICANT: Weich, Nadine S.
 ; APPLICANT: Kelly, Louise M.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
 ; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
 13906,
 ; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
 ; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
 1849,
 ; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
 ; FILE REFERENCE: MPI02-019P1RNOMNIM
 ; CURRENT APPLICATION NUMBER: US/10/352,684A
 ; CURRENT FILING DATE: 2003-01-28
 ; PRIOR APPLICATION NUMBER: US 60/354,333
 ; PRIOR FILING DATE: 2002-02-04
 ; PRIOR APPLICATION NUMBER: US 60/360,258
 ; PRIOR FILING DATE: 2002-02-28
 ; PRIOR APPLICATION NUMBER: US 60/364,476
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/375,626
 ; PRIOR FILING DATE: 2002-04-26
 ; PRIOR APPLICATION NUMBER: US 60/386,494
 ; PRIOR FILING DATE: 2002-06-06
 ; PRIOR APPLICATION NUMBER: US 60/390,965
 ; PRIOR FILING DATE: 2002-06-24
 ; PRIOR APPLICATION NUMBER: US 60/392,480
 ; PRIOR FILING DATE: 2002-06-28
 ; PRIOR APPLICATION NUMBER: US 60/394,128
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/399,783
 ; PRIOR FILING DATE: 2002-07-31
 ; PRIOR APPLICATION NUMBER: US 60/403,221
 ; PRIOR FILING DATE: 2002-08-13
 ; Remaining Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 62
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 22
 ; LENGTH: 425
 ; TYPE: PRT
 ; ORGANISM: Homo Sapiens
 US-10-352-684A-22

Query Match 97.7%; Score 1903; DB 14; Length 425;
 Best Local Similarity 100.0%; Pred. No. 5.1e-173;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMVGPPGSRPSVPPDYEDFLRYLWRDYLKPKQYEWVLIAAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSATPGAQMVGPPGSRPSVPPDYEDFLRYLWRDYLKPKQYEWVLIAAYVAVFVVA 60

Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
 |||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180
 |||
 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSLGIWAVSLAIMVPQA 180

Qy 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
 |||
 Db 181 AVMECSSVLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||
 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy 301 MVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||
 Db 301 MVLVLFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 11

US-09-826-509-549

; Sequence 549, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 549

; LENGTH: 425

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-826-509-549

Query Match 97.5%; Score 1898; DB 10; Length 425;

Best Local Similarity 99.7%; Pred. No. 1.5e-172;

Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60

```

      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPKQYEWVLIAAYVAVFVVA 60

Qy      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSilGIWAVSLAIMVPQA 180

Qy      181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTKKML 300

Qy      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      301 MVLVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy      361 LSG 363
      |||
Db      361 LSG 363

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RESULT 12

US-10-077-874-2

; Sequence 2, Application US/10077874

; Publication No. US20020115155A1

; GENERAL INFORMATION:

; APPLICANT: Soppet, Daniel et al

; TITLE OF INVENTION: Human Neuropeptide Receptor

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: MD

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/077,874

; FILING DATE: 20-Feb-2002

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/462,509

; FILING DATE: 05-JUNE-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Wales, Michele M.

```

;      REGISTRATION NUMBER: 43,975
;      REFERENCE/DOCKET NUMBER: PF168PID1
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 301-309-8504
;      TELEFAX: 301-309-8439
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 402 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-077-874-2

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Query Match          97.4%; Score 1897; DB 13; Length 402;
Best Local Similarity 99.7%; Pred. No. 1.8e-172;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWAVSLAIMVQA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWAVSLAIMVQA 180

Qy    181 AVMECSSLPELANRTRLF SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AVMECSSLPELANRTRLF SVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 KLWGRQIPGTT SALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
        |||
Db    361 LSG 363

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RESULT 13

US-09-961-848-2

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; Sequence 2, Application US/09961848
; Patent No. US20020146719A1
; GENERAL INFORMATION:
; APPLICANT: Berglind Ran Olafsdottir
; APPLICANT: Jeffrey Gulcher
; TITLE OF INVENTION: HUMAN NARCOLEPSY GENE
; FILE REFERENCE: 2345.1005-004
; CURRENT APPLICATION NUMBER: US/09/961,848

```


; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: US 09/479,128
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: US 09/379,083
; PRIOR FILING DATE: 1999-08-23
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-961-848-2

Query Match 97.4%; Score 1897; DB 9; Length 425;
Best Local Similarity 99.7%; Pred. No. 1.9e-172;
Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60
          |||
Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180
          |||
Db    121 VIPYLQAVSVSAVLTLFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
          |||
Db    181 AVMECSSLPELANRTRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
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Db    361 LSG 363
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RESULT 14

US-09-393-696-2

; Sequence 2, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Human Neuropeptide Receptor
; FILE REFERENCE: PF168P2
; CURRENT APPLICATION NUMBER: US/09/393,696
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: PCT/US95/05616

; EARLIER FILING DATE: 1995-06-05
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 369
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-393-696-4

Query Match 96.3%; Score 1875; DB 10; Length 369;
Best Local Similarity 98.6%; Pred. No. 2e-170;
Matches 358; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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Db      1 MEPSATPGAQMGVPPGSREPSVPPDYEDFLRYLWRDYLYPEKQYEWVLIAAYVAVFVVA 60

Qy     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120
          |||
Db     61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFQHALCK 120

Qy    121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180
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Db    121 VIPYLQAVSVSVAVLTLSFIPLDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQA 180

Qy    181 AVMECSSLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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Db    181 AVMQSSSVLPELANRTRLFSLCHERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

Qy    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
          |||
Db    241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300

Qy    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
          |||
Db    301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

Qy    361 LSG 363
          |||
Db    361 LSG 363
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Search completed: October 14, 2004, 11:16:37
Job time : 71.2316 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2004, 10:41:50 ; Search time 97.6261 Seconds
(without alignments)
2192.441 Million cell updates/sec

Title: US-10-070-532-6
Perfect score: 1947
Sequence: 1 MEPSATPGAQMGMVPPGSREP.....ANPIIYNFLSGCKEKS LVLS 372

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		Length	DB	ID	Description
		Match	Length				
1	1903	97.7	425	1	OX1R	HUMAN	O43613 homo sapien
2	1897	97.4	425	2	Q9HBV6		Q9hbv6 homo sapien
3	1783	91.6	416	1	OX1R	RAT	P56718 rattus norv
4	1781	91.5	416	2	Q6VNS3		Q6vns3 mus musculu
5	1781	91.5	416	2	AAR01326		Aar01326 mus muscu
6	1347.5	69.2	444	1	OX2R	CANFA	Q9tup7 canis famil
7	1343.5	69.0	443	2	Q6VLX3		Q6vlx3 mus musculu
8	1343.5	69.0	443	2	AAR01327		Aar01327 mus muscu
9	1343.5	69.0	443	2	AAR11294		Aar11294 mus muscu
10	1343.5	69.0	460	1	OX2R	MOUSE	P58308 mus musculu
11	1343.5	69.0	460	2	AAR01328		Aar01328 mus muscu
12	1343.5	69.0	460	2	AAR11293		Aar11293 mus muscu
13	1342.5	69.0	460	1	OX2R	RAT	P56719 rattus norv
14	1341.5	68.9	444	1	OX2R	HUMAN	O43614 homo sapien
15	1341.5	68.9	444	2	AAG28021		Aag28021 homo sapi

16	1285	66.0	364	2	Q8BV78	Q8bv78 mus musculu
17	1127	57.9	260	1	OX1R_MOUSE	P58307 mus musculu
18	972	49.9	199	2	Q80T45	Q80t45 mus musculu
19	659.5	33.9	166	2	Q8MJ13	Q8mj13 ovis aries
20	614	31.5	127	2	Q8SPR4	Q8spr4 ovis aries
21	533	27.4	109	2	Q8I010	Q8i010 bos taurus
22	485.5	24.9	430	1	NFF1_HUMAN	Q9gzq6 homo sapien
23	483	24.8	417	1	NFF2_MOUSE	Q924h0 mus musculu
24	480.5	24.7	432	1	NFF1_RAT	Q9ep86 rattus norv
25	479.5	24.6	405	2	Q924N0	Q924n0 mus musculu
26	476.5	24.5	522	1	NFF2_HUMAN	Q9y5x5 homo sapien
27	472	24.2	417	1	NFF2_RAT	Q9eqd2 rattus norv
28	463.5	23.8	399	2	Q75XU5	Q75xu5 gallus gall
29	463.5	23.8	399	2	BAC87782	Bac87782 gallus ga
30	453	23.3	432	2	Q924G9	Q924g9 rattus norv
31	443.5	22.8	758	2	Q7YU49	Q7yu49 drosophila
32	437	22.4	86	1	OX1R_PIG	O97661 sus scrofa
33	427.5	22.0	464	2	Q9VB87	Q9vb87 drosophila
34	427.5	22.0	464	2	AAF56655	Aaf56655 drosophil
35	422.5	21.7	449	1	NYR_DROME	P25931 drosophila
36	420.5	21.6	375	2	O57463	O57463 brachydanio
37	420	21.6	353	2	Q7PRC5	Q7prc5 anopheles g
38	417	21.4	370	2	Q6VMN6	Q6vmn6 mus musculu
39	417	21.4	370	2	AAQ84215	Aaq84215 mus muscu
40	415	21.3	382	1	NY2R_PIG	O02836 sus scrofa
41	413.5	21.2	370	1	GP10_RAT	Q64121 rattus norv
42	413	21.2	370	1	GP10_HUMAN	P49683 homo sapien
43	409	21.0	517	2	Q9VWR3	Q9vwr3 drosophila
44	407.5	20.9	542	2	Q9VRM0	Q9vrm0 drosophila
45	407.5	20.9	542	2	AAF50775	Aaf50775 drosophil

ALIGNMENTS

RESULT 1

OX1R_HUMAN

ID OX1R_HUMAN STANDARD; PRT; 425 AA.

AC O43613;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).

GN Name=HCRTR1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=98150861; PubMed=9491897;

RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,

RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,

RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,

RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,

RA Yanagisawa M.;

RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides

RT and G protein-coupled receptors that regulate feeding behavior.";
 RL Cell 92:573-585(1998)..
 RN [2]
 RP REVIEW.
 RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
 RA Hungs M., Mignot E.;
 RT "Hypocretin/orexin, sleep and narcolepsy.";
 RL Bioessays 23:397-408(2001).
 RN [3]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
 CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
 CC exclusively coupled to the G(q) subclass of heteromeric G
 CC proteins, which activates the phospholipase C mediated signaling
 CC cascade (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF041243; AAC39601.1; -.
 DR Genew; HGNC:4848; HCRTR1.
 DR MIM; 602392; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0004930; F:G-protein coupled receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane.
 FT DOMAIN 1 46 Extracellular (Potential).
 FT TRANSMEM 47 67 1 (Potential).
 FT DOMAIN 68 80 Cytoplasmic (Potential).
 FT TRANSMEM 81 102 2 (Potential).
 FT DOMAIN 103 119 Extracellular (Potential).
 FT TRANSMEM 120 142 3 (Potential).
 FT DOMAIN 143 164 Cytoplasmic (Potential).
 FT TRANSMEM 165 185 4 (Potential).
 FT DOMAIN 186 216 Extracellular (Potential).

FT TRANSMEM 217 239 5 (Potential).
 FT DOMAIN 240 298 Cytoplasmic (Potential).
 FT TRANSMEM 299 321 6 (Potential).
 FT DOMAIN 322 336 Extracellular (Potential).
 FT TRANSMEM 337 360 7 (Potential).
 FT DOMAIN 361 425 Cytoplasmic (Potential).
 FT CARBOHYD 194 194 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 425 AA; 47521 MW; 1634083DE10CA092 CRC64;

Query Match 97.7%; Score 1903; DB 1; Length 425;
 Best Local Similarity 100.0%; Pred. No. 3.2e-120;
 Matches 363; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60
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 Db 1 MEPSATPGAQMGPVPPGSREPSVPVPPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
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 Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
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 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQA 180
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 Qy 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQ IFR 240
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 Db 181 AVMECSSLPELANRTRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQ IFR 240
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 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
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 Qy 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
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 Db 301 MVVLLVFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
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 Qy 361 LSG 363
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 Db 361 LSG 363

RESULT 2

Q9HBV6

ID Q9HBV6 PRELIMINARY; PRT; 425 AA.
 AC Q9HBV6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypocretin receptor-1 (Orexin receptor 1).
 GN Name=HCRTR1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=20429525; PubMed=10973318;
 RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
 RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
 RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
 RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
 RT "A mutation in a case of early onset narcolepsy and a generalized
 RT absence of hypocretin peptides in human narcoleptic brains.";
 RL Nat. Med. 6:991-997(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21580342; PubMed=11723285;
 RA Olafsdottir B.R., Rye D.B., Scammell T.E., Matheson J.K.,
 RA Stefansson K., Gulcher J.R.;
 RT "Polymorphisms in hypocretin/orexin pathway genes and narcolepsy.";
 RL Neurology 57:1896-1899(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Olafsdottir B.R., Stefansson R.H., Sigurdsson A., Hannesson H.H.,
 RA Sainz J., Scammell T.E., Stefansson K., Gulcher J.R.;
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Yeager M., Welch R., Haque K., Bergen A.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pooled tissue;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF202084; AAG28020.1; -.
 DR EMBL; AF202078; AAG28020.1; JOINED.
 DR EMBL; AF202079; AAG28020.1; JOINED.
 DR EMBL; AF202081; AAG28020.1; JOINED.

DR EMBL; AF202083; AAG28020.1; JOINED.
 DR EMBL; AF202082; AAG28020.1; JOINED.
 DR EMBL; AF202080; AAG28020.1; JOINED.
 DR EMBL; AY062030; AAL47214.1; -.
 DR EMBL; AY070269; AAL50221.1; -.
 DR EMBL; BC074796; AAH74796.1; -.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016499; F:orexin receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004059; Orexin_receptor1.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01521; OREXIN1R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 425 AA; 47535 MW; B650B37F3A2CA096 CRC64;

Query Match 97.4%; Score 1897; DB 2; Length 425;
 Best Local Similarity 99.7%; Pred. No. 8.1e-120;
 Matches 362; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MEPSATPGAQMGVPPGSREPSVPDPDYEDFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVA 60

 Qy 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120
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 Db 61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLF GHALCK 120

 Qy 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSI LGIWAVSLAIMVPQA 180
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 Db 121 VIPYLQAVSVSVAVLTLSFIALDRWYAICHPLLEFKSTARRARGSI LGIWAVSLAIMVPQA 180

 Qy 181 AVMECSSLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240
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 Db 181 AVMECSSLPELANRTRLFSCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

 Qy 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
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 Db 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRARAFLAEVKQMRARRKTAKML 300

 Qy 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 MVVLLVFALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

 Qy 361 LSG 363
 |||
 Db 361 LSG 363

RESULT 3

OX1R_RAT

ID OX1R RAT STANDARD; PRT; 416 AA.
AC P56718;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Orexin receptor type 1 (Ox1r) (Hypocretin receptor type 1).
GN Name=Hcrtr1;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98150861; PubMed=9491897;
RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: Moderately selective excitatory receptor for orexin-A
CC and, with a lower affinity, for orexin-B neuropeptide. Seems to be
CC exclusively coupled to the G(q) subclass of heteromeric G
CC proteins, which activates the phospholipase C mediated signaling
CC cascade.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in the brain in the
CC prefrontal cortex, hippocampus, paraventricular thalamus,
CC ventromedial hypothalamus, arcuate nucleus, dorsal raphe nucleus,
CC and locus coeruleus. Not detected in the spleen, lung, liver,
CC skeletal muscle, kidney and testis. Orexin receptor mRNA
CC expression has also been reported in the adrenal gland, enteric
CC nervous system, and pancreas.
CC -!- INDUCTION: By nutritional state, up-regulated by fasting.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way


```

Db      181 AVMECSSVLPELANRTRLSVCDEHWADELYPKIYHSCFFIVTYLAPLGLMGMAFYQIFR 240
QY      241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
Db      241 KLWGRQIPGTTSALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300
QY      301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
Db      301 MVVLLVFALCYLPISVLNVLKRVEGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
QY      361 LSG 363
Db      361 LSG 363

```

RESULT 5

AAR01326

```

ID  AAR01326    PRELIMINARY;      PRT;    416 AA.
AC  AAR01326;
DT  02-MAR-2004 (TrEMBLrel. 27, Created)
DT  02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT  02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE  Orexin receptor type-1.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=BALB/c;
RA  Chen J., Randeve H.S.;
RT  "Cloning and Characterization of the Mouse Type-1 Orexin Receptor
RT  (OX1R).";
RL  Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR  EMBL; AY336083; AAR01326.1; -.
KW  Receptor.
SQ  SEQUENCE    416 AA;  46766 MW;  A8958C594C365E00 CRC64;

```

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Query Match          91.5%;  Score 1781;  DB 2;  Length 416;
Best Local Similarity 93.9%;  Pred. No. 5.1e-112;
Matches 341;  Conservative 6;  Mismatches 16;  Indels 0;  Gaps 0;

```

```

QY      1 MEPSATPGAQMGPVPPGSREPSVPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFVVA 60
Db      1 MEPSATPGAQPGVPTSSGEPFHLPPDYEDFLRYLWRDYLKQYEWVLIAAYVAVFLIA 60
QY      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQHALCK 120
Db      61 LVGNTLVCLAVWRNHHMRTVTNYFIVNLSLADVLTALCLPASLLVDITESWLFQALCK 120
QY      121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAIMVPQA 180
Db      121 VIPYLQAVSVSAVLTLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSLAVMVPQA 180
QY      181 AVMECSSVLPELANRTRLSVCDEHWADELYPKIYHSCFFIVTYLAPLGLMAMAYFQIFR 240

```

Db 181 AVMECSSVLPELANRTRLFSVCDEHWADELYPKIYHSCFFIVTYLAPLGLMGMAFYQIFR 240

QY 241 KLWGRQIPGTTSALVRNWKRPDQLGDLEQGLSGEPQPRGRAFLAEVKQMRARRKTAKML 300
 |||||:| | | | |

Db 241 KLWGRQIPGTTSALVRNWKRPSEQLEAQHQGLCTEPQPRARAFLAEVKQMRARRKTAKML 300

QY 301 MVLVLFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360
 |||||

Db 301 MVLVLFALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNF 360

QY 361 LSG 363
 |||

Db 361 LSG 363

RESULT 6

OX2R_CANFA

ID OX2R_CANFA STANDARD; PRT; 444 AA.

AC Q9TUP7;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).

GN Name=HCRTR2;

OS Canis familiaris (Dog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

OX NCBI_TaxID=9615;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=99385793; PubMed=10458611;

RA Lin L., Faraco J., Li R., Kadotani H., Rogers W., Lin X., Qiu X.,

RA de Jong P.J., Nishino S., Mignot E.;

RT "The sleep disorder canine narcolepsy is caused by a mutation in the

RT hypocretin receptor 2 gene.";

RL Cell 98:365-376(1999).

RN [2]

RP REVIEW.

RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;

RA Hungs M., Mignot E.;

RT "Hypocretin/orexin, sleep and narcolepsy.";

RL Bioessays 23:397-408(2001).

RN [3]

RP REVIEW.

RX MEDLINE=21178476; PubMed=11283317;

RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;

RT "To eat or to sleep? Orexin in the regulation of feeding and

RT wakefulness.";

RL Annu. Rev. Neurosci. 24:429-458(2001).

RN [4]

RP VARIANT NARCOLEPSY LYS-54, AND MUTAGENESIS OF GLU-54.

RX MEDLINE=21180003; PubMed=11282968; DOI=10.1101/gr.161001;

RA Hungs M., Fan J., Lin L., Lin X., Maki R.A., Mignot E.;

RT "Identification and functional analysis of mutations in the hypocretin

RT (orexin) genes of narcoleptic canines.";

RL Genome Res. 11:531-539(2001).

CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A

CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- DISEASE: Defects in HCRT2 are a cause of an autosomal recessive
 CC form of narcolepsy, observed in labradors, dobermans and
 CC dachshunds. Narcolepsy is a neurological sleep disorder affecting
 CC animals and humans, characterized by excessive daytime sleepiness,
 CC sleep fragmentation, symptoms of abnormal rapid-eye-movement
 CC (REM) sleep, such as cataplexy, hypnagogic hallucinations, and
 CC sleep paralysis. Cataplexy is a sudden loss of muscle tone
 CC triggered by emotions, which is the most valuable clinical feature
 CC used to diagnose narcolepsy. As in humans, most cases of canine
 CC narcolepsy are sporadic but an autosomal recessive form was also
 CC observed.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF164626; AAD49333.1; -.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW Disease mutation; G-protein coupled receptor; Glycoprotein;
 KW Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 FT VARIANT 54 54 E -> K (in autosomal recessive
 FT narcolepsy).
 FT MUTAGEN 54 54 E->K: Loss of function.
 SQ SEQUENCE 444 AA; 50675 MW; D848A4536D485D6B CRC64;

DR EMBL; AY336084; AAR01327.1; -.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR000923; BlueCu_1.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PRINTS; PR01064; OREXINR.
 DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Receptor; Transmembrane-
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17	SREPSVPPDYED-EFLRYLWRDYLYPKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		: : : : : : : : :		
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES	WLFHALCKVIPYLQAVSVSVAVL	135
		: : : : : : : :		
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITET	WFFGQSLCKVIPYLQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVSL	AIMVPPQAAVMECSSLPELANR	195
		: : : : : : :		
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNIVVIWIVSCI	IMIPQAIVMECSSLPLGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLM	AMAYFQIFRWGRQIPGTTSALV	255
		: : : : : : : : :		
Db	204	TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLM	ILAYLQIFRWGRQIPGTSSVVQ	263
Qy	256	RNWKRPDQLGDLQGLSGEPQPRG-----RAFLAEV	KQMRARRKTAKMLMVLLV	306
		: : : : : :		
Db	264	RKWKQ-----QQPVS---QPRGSGQQSKARISAV	AAEIKQIRARRKTARMLMVLLV	312
Qy	307	FALCYLPISVLNVLKRIVFGMFRQASDREAVYACFT	FSHWLVYANSAANPIYNFLSG	363
		: :		
Db	313	FAICYLPISILNVLKRIVFGMFTHTEDRETVEYAWF	TFSHWLTVYANSAANPIYNFLSG	369

RESULT 8
 AAR01327

ID AAR01327 PRELIMINARY; PRT; 443 AA.
 AC AAR01327;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Chen J., Randeve H.S.;
 RT "Cloning and Characterization of the Mouse Type-2a Orexin Receptor
 RT Subtype (OX2aR).";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY336084; AAR01327.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy 17 SREPSVPPDYED-EFLRYLWRDYLKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
 :|| | ||:| |||||:|:|:| |||| | : ||||:| | ||:|:|
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
 Qy 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFHGHALCKVIPYQLQAVSVSVAVL 135
 ||||| ||||| ||||:| ||||:| || : ||||| ||||:|
 Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYQLQTVSVSVSVL 143
 Qy 136 TLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQAAMVMECSSLPELANR 195
 ||| ||||| ||||:| ||| ||: || || : ||| ||||:| ||:
 Db 144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVVIWIVSCIIMIPQAIVMECSSLPLGLANK 203
 Qy 196 TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALV 255
 | ||: ||| | : |||:| |||: ||| || : || ||||| ||||:| :
 Db 204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSV VQ 263
 Qy 256 RNWKRPDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
 | ||: : | :| ||| | ||: ||: |||||: |||||
 Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312
 Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
 ||: |||||: ||||| || || ||||| ||||| |||||
 Db 313 FAICYLPISILNVLKRVFGMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 9

AAR11294

ID AAR11294 PRELIMINARY; PRT; 443 AA.
 AC AAR11294;
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
 DE Orexin receptor type-2a.
 GN MOXR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;

RA Chen J., Randeve H.S.;
 RT "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
 RT gene.";
 RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY339383; AAR11294.1; JOINED.
 DR EMBL; AY339384; AAR11294.1; JOINED.
 DR EMBL; AY339385; AAR11294.1; JOINED.
 DR EMBL; AY339386; AAR11294.1; JOINED.
 DR EMBL; AY339387; AAR11294.1; JOINED.
 DR EMBL; AY339388; AAR11294.1; JOINED.
 DR EMBL; AY339389; AAR11294.1; -.
 KW Receptor.
 SQ SEQUENCE 443 AA; 50559 MW; 794736A669463283 CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 443;
 Best Local Similarity 71.7%; Pred. No. 1.5e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17	SREPSVPDPDYED-EFLRYLWRDYLYPKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		:	: : : : :	: : :
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDIT	ESWLFHGHALCKVIPYLQAVSVSVAVL	135
			: : : : :	:
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDIT	ETWFFGQSLCKVIPYLQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWA	VSLAIMVPQAAMVMECSSVLPELANR	195
			: : : : : : : :	
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIW	IVSCIIMIPQAIVMECSSMLPGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGL	MAMAYFQIFRKLWGRQIPGTTTSALV	255
		:	: : : : :	: :
Db	204	TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCL	MILAYLQIFRKLWCRQIPGTSSVVQ	263
Qy	256	RNWKRPDQGLGDLEQGLSGEPQPRG-----	RAFLAEVKQMRARRKTAKMLMVLLV	306
		:	: : : : :	
Db	264	RKWKQ-----QQPVS---QPRGSGQQSKARISAV	AAEIKQIRARRKTARMLMVLLV	312
Qy	307	FALCYLPISVLNVLKRVFGMFRQASDREAVYACFT	FSHWLVYANSAANPIIYNFLSG	363
		: :		
Db	313	FAICYLPISILNVLKRVFGMETHTEDRETVEYAWFT	FSHWLVYANSAANPIIYNFLSG	369

RESULT 10

OX2R_MOUSE

ID OX2R_MOUSE STANDARD; FRT; 460 AA.
 AC P58308; Q8BG12;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
 GN Name=Hcrtr2; Synonyms=Mox2r;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Cerebellum, and Hypothalamus;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA Kanai A., Kawaji H., Kawasaki Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA Birney E., Hayashizaki Y.;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [2]
RP SEQUENCE OF 100-311 FROM N.A.
RC STRAIN=C57BL/6;
RA Szendro P.I., Maevers K., Eichele G.;
RT "Cloning of mouse orexin receptors.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN [3]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [4]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
CC and orexin-B neuropeptides.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
CC -----
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 CC or send an email to license@isb-sib.ch).

 DR EMBL; AK038551; BAC30039.1; -.
 DR EMBL; AK048781; BAC33457.1; -.
 DR EMBL; AF394597; AAK71327.1; -.
 DR MGD; MGI:1889024; Mox2r.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 460 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 FT CONFLICT 201 201 A -> T (in Ref. 2).
 FT CONFLICT 240 240 I -> V (in Ref. 2).
 SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 69.0%; Score 1343.5; DB 1; Length 460;
 Best Local Similarity 71.7%; Pred. No. 1.6e-82;
 Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

QY 17 SREPSPVPPDYED-EFLRYLWRDYLYPEKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
 :|| | ||:| |||||:|:|:| ||||| |: |||||:| |||:|:|:
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
 QY 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFEGHALCKVIPYLQAVSVSVAVL 135
 |||||:|:|:|:| |||:|:|:|:| ||:|:|:| ||||:|:
 Db 84 HMRTVTNYFIVNLSLADVLVTTCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143
 QY 136 TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPQAAMVMECSSLPELANR 195
 ||| |||||:|:|:|:| ||:| || ||:| |||||:| |||:

Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSLMLPGLANK 203

QY 196 TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
| ||:|||| | :|||:| | ||:|||| | | :| | ||||| | ||||:| :

Db 204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263

QY 256 RNWKRPDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
| ||: :| :| ||| | ||:| | |||||:|||||||

Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312

QY 307 FALCYLPISVLNVLKRVFQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
||:|||||:||||||| || || |||||:|||||||

Db 313 FAICYLPISILNVLKRVFQMFTHTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSG 369

RESULT 11

AAR01328

ID AAR01328 PRELIMINARY; PRT; 460 AA.

AC AAR01328;

DT 02-MAR-2004 (TrEMBLrel. 27, Created)

DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)

DE Orexin receptor type-2b.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=BALB/c;

RA Chen J., Randeve H.S.;

RT "Cloning and Characterization of the Mouse Type-2b Orexin Receptor

RT Subtype (OX2bR).";

RL Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY336085; AAR01328.1; -.

KW Receptor.

SQ SEQUENCE 460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

Query Match 69.0%; Score 1343.5; DB 2; Length 460;

Best Local Similarity 71.7%; Pred. No. 1.6e-82;

Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

QY 17 SREPSVPDPDYED-EFLRYLWRDYLYPEQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
::|| | ||:| |||||:| | ||:|||| | : |||||:| | ||:| | |

Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

QY 76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLAQVSVSVAVL 135
|||||||:|||||:| || :||||||| ||||:| |

Db 84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLAQVSVSVSL 143

QY 136 TLSFIALDRWYAICHPLLFKSTARRARGSI LGIWA VSLAIMVPQAAMVMECSSLPELANR 195
||| |||||:||||:| | ||:| | ||||:| | ||:

Db 144 TLSCIALDRWYAICHPLMFKSTAKRARNISIVVIWIVSCIIMIPQAIVMECSSLMLPGLANK 203

QY 196 TRLFVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTTSALV 255
| ||:|||| | :|||:| | ||:|||| | | :| | ||||| | ||||:| :

Db 204 TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQ 263

Qy 256 RNWKRPSDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
| ||: : | || | | ||: ||: |||||: |||||
Db 264 RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV 312

Qy 307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
||:|||||:||||| || | || | |||||
Db 313 FAICYLPISILNVLKRVFGMTHTEDRETVEAWETFSHWLVYANSAANPIIYNFLSG 369

RESULT 12

AAR11293

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ID      AAR11293      PRELIMINARY;      PRT;      460 AA.
AC      AAR11293;
DT      02-MAR-2004 (TrEMBLrel. 27, Created)
DT      02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT      02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE      Orexin receptor type-2b.
GN      MOXR2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BALB/c;
RA      Chen J., Randeve H.S.;
RT      "Genomic structure analysis of the Mus musculus orexin type-2 (MOXR2)
RT      gene.";
RL      Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AY339383; AAR11293.1; JOINED.
DR      EMBL; AY339384; AAR11293.1; JOINED.
DR      EMBL; AY339385; AAR11293.1; JOINED.
DR      EMBL; AY339386; AAR11293.1; JOINED.
DR      EMBL; AY339387; AAR11293.1; JOINED.
DR      EMBL; AY339388; AAR11293.1; JOINED.
DR      EMBL; AY339389; AAR11293.1; JOINED.
DR      EMBL; AY339390; AAR11293.1; -.
KW      Receptor.
SO      SEQUENCE      460 AA; 52461 MW; D62A67C15BA67DCC CRC64;

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Query Match 69.0%; Score 1343.5; DB 2; Length 460;
Best Local Similarity 71.7%; Pred. No. 1.6e-82;
Matches 256; Conservative 38; Mismatches 42; Indels 21; Gaps 4;

Qy	17	SREPSFVPPDYED-EFLRLYLWRDYLYPEKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH	75
		:: : : : : : : : : : : :	
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLAQAVSVSVAVL	135
		: : : : : : :	
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLAQAVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRARGSILGIWAVSLAIMVPPAAVMECSSLPELANR	195
		: : : : : : : : :	
Db	144	TLSCIALDRWYAICHPLMEFKSTAKRARNISIVVIWIVSCIIMIPQATVMECSSLPLGLANK	203

QY	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGMLMAMAYFQIFRKLWGRQIPGTTSA	LV	255
Db	204	TTLFTVCDEHWGGEVYPKMYHICFFLVTYMAPLCMLLAYLQIFRKLWCRQIPGTSSVVQ		263
QY	256	RNWKRPDQLGDLEQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV		306
Db	264	RKWKQ-----QQPVS---QPRGSGQQSKARISAVAAEIKQIRARRKTARMLMVLLV		312
QY	307	FALCYLPISVLNVLKRVFGMFQRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG		363
Db	313	FAICYLPISILNVLKRVFGMFTHTEDRETVEAWFTFSHWLVYANSAANPIIYNFLSG		369

RESULT 13

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OX2R_RAT
ID OX2R RAT STANDARD; PRT; 460 AA.
AC P56719;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Orexin receptor type 2 (Ox2r) (Hypocretin receptor type 2).
GN Name=Hcrtr2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98150861; PubMed=9491897;
RA Sakurai T., Amemiya A., Ishii M., Matsuzaki I., Chemelli R.M.,
RA Tanaka H., Williams S.C., Richardson J.A., Kozlowski G.P., Wilson S.,
RA Arch J.R.S., Buckingham R.E., Haynes A.C., Carr S.A., Annan R.S.,
RA McNulty D.E., Liu W.-S., Terrett J.A., Elshourbagy N.A., Bergsma D.J.,
RA Yanagisawa M.;
RT "Orexins and orexin receptors: a family of hypothalamic neuropeptides
RT and G protein-coupled receptors that regulate feeding behavior.";
RL Cell 92:573-585(1998).
RN [2]
RP REVIEW.
RX MEDLINE=21237974; PubMed=11340621; DOI=10.1002/bies.1058;
RA Hungs M., Mignot E.;
RT "Hypocretin/orexin, sleep and narcolepsy.";
RL Bioessays 23:397-408(2001).
RN [3]
RP REVIEW.
RX MEDLINE=21178476; PubMed=11283317;
RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
RT "To eat or to sleep? Orexin in the regulation of feeding and
RT wakefulness.";
RL Annu. Rev. Neurosci. 24:429-458(2001).
CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
CC and orexin-B neuropeptides.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed in the brain in the cerebral cortex,
CC septal nuclei, hippocampus, medial thalamic groups, dorsal and
CC median raphe nuclei, and many hypothalamic nuclei including the

```


CC tuberomammillary nucleus, dorsomedial hypothalamus,
 CC paraventricular hypothalamic nucleus, and ventral premammillary
 CC nucleus. Not detected in the spleen, lung, liver, skeletal muscle,
 CC kidney and testis. Orexin receptor mRNA expression has also been
 CC reported in the adrenal gland, enteric nervous system, and
 CC pancreas.
 CC -- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041246; AAC40042.1; -.
 DR RGD; 2788; Hcrtr2.
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 460 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc. . .) (Potential).
 SQ SEQUENCE 460 AA; 52489 MW; 3B44E3D82F8B85D5 CRC64;

Query Match 69.0%; Score 1342.5; DB 1; Length 460;
 Best Local Similarity 72.0%; Pred. No. 1.8e-82;
 Matches 257; Conservative 37; Mismatches 42; Indels 21; Gaps 4;

QY 17 SREPSVPPDYED-EFLRYLWRDYLYPKQYEWVLIAAYVAVFVVALVGNTLVCLAVWRNH 75
 Db 24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83
 QY 76 HMRTVTNYFIVNLSLADVLTVAICLPASLLVDITESWLFQHALCKVIPYLQAVSVSVAVL 135

RN [4]
 RP REVIEW.
 RX MEDLINE=21178476; PubMed=11283317;
 RA Willie J.T., Chemelli R.M., Sinton C.M., Yanagisawa M.;
 RT "To eat or to sleep? Orexin in the regulation of feeding and
 RT wakefulness.";
 RL Annu. Rev. Neurosci. 24:429-458(2001).
 CC -!- FUNCTION: Nonselective, high-affinity receptor for both orexin-A
 CC and orexin-B neuropeptides.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 CC -----
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 CC -----
 DR EMBL; AF041245; AAC39602.1; -.
 DR EMBL; AY062031; AAL47215.1; -.
 DR Genew; HGNC:4849; HCRT2.
 DR MIM; 602393; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0008188; F:neuropeptide receptor activity; TAS.
 DR GO; GO:0007631; P:feeding behavior; TAS.
 DR GO; GO:0007218; P:neuropeptide signaling pathway; TAS.
 DR GO; GO:0007268; P:synaptic transmission; TAS.
 DR InterPro; IPR000276; GPCR Rhodpsn.
 DR InterPro; IPR000204; Orexin_receptor.
 DR InterPro; IPR004060; Orexin_receptor2.
 DR Pfam; PF00001; 7tm_1; 1.
 DR Pfam; PF03827; Orexin_rec2; 1.
 DR PRINTS; PR00237; GPCRRHODOPSN.
 DR PRINTS; PR01522; OREXIN2R.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 54 Extracellular (Potential).
 FT TRANSMEM 55 75 1 (Potential).
 FT DOMAIN 76 88 Cytoplasmic (Potential).
 FT TRANSMEM 89 110 2 (Potential).
 FT DOMAIN 111 127 Extracellular (Potential).
 FT TRANSMEM 128 150 3 (Potential).
 FT DOMAIN 151 172 Cytoplasmic (Potential).
 FT TRANSMEM 173 193 4 (Potential).
 FT DOMAIN 194 224 Extracellular (Potential).
 FT TRANSMEM 225 247 5 (Potential).
 FT DOMAIN 248 304 Cytoplasmic (Potential).
 FT TRANSMEM 305 327 6 (Potential).
 FT DOMAIN 328 342 Extracellular (Potential).
 FT TRANSMEM 343 366 7 (Potential).
 FT DOMAIN 367 444 Cytoplasmic (Potential).
 FT CARBOHYD 14 14 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 22 22 N-linked (GlcNAc . . .) (Potential).
 FT CARBOHYD 202 202 N-linked (GlcNAc . . .) (Potential).

SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 68.9%; Score 1341.5; DB 1; Length 444;
Best Local Similarity 71.4%; Pred. No. 2.1e-82;
Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

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Qy      17 SREPSVPFPDYED-EFLRYLWRDYLYPKQYEWVLI AAYVAVFVVALVGNTLVCLAVWRNH 75
          ::|| | ||:| |||||:|:|:| ||||| | : |||||:| | ||:|:|:|
Db      24 TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLIAGYIIVFVVALIGNVLVCVAVWKNH 83

Qy      76 HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITESWLFGHALCKVIPYLQAVSVSVAVL 135
          ||||| ||||| |||||:|:|:| | | : ||||| |||||:|
Db      84 HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITETWFFGQSLCKVIPYLQTVSVSVSVL 143

Qy     136 TLSFIALDRWYAICHPLLFKSTARRARSGILGIWAVSLAIMVPQAAMVECSSVLPELANR 195
          || | ||||| |||||:|:|:| || | | | : || | |||||:| | ||:
Db     144 TLSCIALDRWYAICHPLMFKSTAKRARN SIVIIWIVSCIIMIPQAIVMECSTVFPGLANK 203

Qy     196 TRLFVSVCDERWADDLYPKIYHSCFFIVTYLAPLGLMAMAYFQIFRKLWGRQIPGTT SALV 255
          | ||:| |||| | : ||:| | ||:|:|:| | | : || ||||| | ||||:| :
Db     204 TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLCLMVLAYLQIFRKLWCRQIPGTSSVVQ 263

Qy     256 RNWKRPDQLGDLQGLSGEPQPRG-----RAFLAEVKQMRARRKTAKMLMVLLV 306
          | || | | | | | | | | | | | | | | | | | | | | | | | | |
Db     264 RKWK-----PLQPVSQPRGPGQPTKSRMSAVAAEIKQIRARRKTARMLMVLLV 312

Qy     307 FALCYLPISVLNVLKRVFGMFRQASDREAVYACFTFSHWLVYANSAANPIIYNFLSG 363
          ||:|||||:||||| || | || | ||||| ||||| ||||| ||||| |||||
Db     313 FAICYLPISILNVLKRVFGMFAHTEDRET VYAWFTFSHWLVYANSAANPIIYNFLSG 369
```

RESULT 15

AAG28021

ID AAG28021 PRELIMINARY; PRT; 444 AA.
AC AAG28021;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypocretin receptor-2.
GN HCRTR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20429525; PubMed=10973318;
RA Peyron C., Faraco J., Rogers W., Ripley B., Overeem S., Charnay Y.,
RA Nevsimalova S., Aldrich M., Reynolds D., Albin R., Li R., Hungs M.,
RA Pedrazzoli M., Padigaru M., Kucherlapati M., Fan J., Maki R.,
RA Lammers G.J., Bouras C., Kucherlapati R., Nishino S., Mignot E.;
RT "A mutation in a case of early onset narcolepsy and a generalized
RT absence of hypocretin peptides in human narcoleptic brains.";
RL Nat. Med. 6:991-997(2000).
DR EMBL; AF202091; AAG28021.1; -.
DR EMBL; AF202085; AAG28021.1; JOINED.
DR EMBL; AF202086; AAG28021.1; JOINED.

DR EMBL; AF202087; AAG28021.1; JOINED.
 DR EMBL; AF202088; AAG28021.1; JOINED.
 DR EMBL; AF202089; AAG28021.1; JOINED.
 DR EMBL; AF202090; AAG28021.1; JOINED.
 KW Receptor.
 SQ SEQUENCE 444 AA; 50680 MW; CA0669F0D4224C65 CRC64;

Query Match 68.9%; Score 1341.5; DB 2; Length 444;
 Best Local Similarity 71.4%; Pred. No. 2.1e-82;
 Matches 255; Conservative 35; Mismatches 46; Indels 21; Gaps 3;

Qy	17	SREPSVPPDYED-EFLRYLWRDYLYPEKQYEWVLI	AAYVAVFVVALVGNTLVCLAVWRNH	75
		:	: : : :	: : : :
Db	24	TQEPFLNPTDYDDEEFLRYLWREYLHPKEYEWVLI	AGYIIVFVVALIGNVLVCVAVWKNH	83
Qy	76	HMRTVTNYFIVNLSLADVLVTAICLPASLLVDITES	WLFHALCKVIPYQLQAVSVSVAVL	135
			: : : :	:
Db	84	HMRTVTNYFIVNLSLADVLVTITCLPATLVVDITET	WFFGQSLCKVIPYQLQTVSVSVSVL	143
Qy	136	TLSFIALDRWYAICHPLLFKSTARRAGSILGIWAVS	LAIMVPQAAMVMECSSLPELANR	195
			: : : : : :	
Db	144	TLSCIALDRWYAICHPLMFKSTAKRARNIVIIWIVS	CIIMIPQAIVMECSTVFPGLANK	203
Qy	196	TRLFSVCDERWADDLYPKIYHSCFFIVTYLAPLGL	MAMAYFQIFRWGRQIPGTTSALV	255
		:	: : : : :	: :
Db	204	TTLFTVCDERWGGEIYPKMYHICFFLVTYMAPLC	LMVLAYLQIFRWLWCRQIPGTSSVVQ	263
Qy	256	RNWKRPDQLGDLQGLSGEPQPRG-----	RAFLAEVKQMRARRKTAKMLMVLLV	306
				: : :
Db	264	RKWK-----	PLQPVSQPRGPGQPTKSRMSAVAAEIKQIRARRKT	ARMLMVLLV 312
Qy	307	FALCYLPISVLNVLKRFGMFRQASDREAVYACFTF	SHWLVIYANSAANPIYNFLSG	363
		: :		
Db	313	FAICYLPISILNVLKRFGMFAHTEDRETVYAWFTF	SHWLVIYANSAANPIYNFLSG	369

Search completed: October 14, 2004, 10:55:50
 Job time : 98.6261 secs